

TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GTATGGGAAT 60  
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120  
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180  
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCh 240  
 CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300  
 10 TnTTCAGCTG 310

## (2) INFORMATION FOR SEQ ID NO: 3198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60  
 25 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120  
 AATTGAATCA GCTTTTnTCG 140

## (2) INFORMATION FOR SEQ ID NO: 3199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

40 TGGTGATTTC AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAT TATTTGTTG 60  
 TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTTGTTAA 120  
 45 AACCAGTGAT TGCAACCTGC CATTCAcAnG GAAAATTACC TAATAAGTGG CGTATTTACC 180  
 AGTC 184

## (2) INFORMATION FOR SEQ ID NO: 3200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60  
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTGTC 120  
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

## (2) INFORMATION FOR SEQ ID NO: 3201:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

20 GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60  
 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAGATA CGTAATGTnT 120  
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

## (2) INFORMATION FOR SEQ ID NO: 3202:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

35 CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAACTGT 60  
 AAAACGAGTG AATTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120  
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180  
 AAAGTCCGAT TC 192

## (2) INFORMATION FOR SEQ ID NO: 3203:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTTGT ATTCGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAGC 120  
 ATCTTATAGC GTGATAGCCA TCGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180  
 5 TAAGCAGTAC ACACCAGTAA CATTTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGTTATCA TCCTCTCTTA ATGACTATCT 60  
 20 TTAAATTACG NAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120  
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTGTGTC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TGCGCATTAT 60  
 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACCTTCAGTG CTTACTGGnT 120  
 CATCTAAATG ATTTTtagCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60  
 GACTTTCAGT CGTAACGTTT ACAAactTAA GCGCACGTCA nATGAAGCAT CGTGTAGACC 120

## (2) INFORMATION FOR SEQ ID NO: 3207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60  
 AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GntTAATGAA TGCATTAAGA 120  
 AGCTGCAAGA ACTTATAAGT GTGCA 145

## (2) INFORMATION FOR SEQ ID NO: 3208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnAAT CACACTTAGC 60  
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTTATCAA CGGTATATGA AGGGGATTG 120  
 GAAGATGCGT T 131

## (2) INFORMATION FOR SEQ ID NO: 3209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60  
 CCCGCATCCA TTGTAAATA ACACGGATAC CCCGCTTCTC GGCATTCTGT AACAGCGCCA 120  
 TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

## (2) INFORMATION FOR SEQ ID NO: 3210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

	AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC	60
10	AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC	120
	AACCTGGTGG GTATTGTGAT TAT	143

(2) INFORMATION FOR SEQ ID NO: 3211:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

25	ATGCATACTG TATGTGTTCC AGCATATACA ATTTTnCCA TCTTTAATGA CAACTGTACC	60
	ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCCTC AAAGTTTATC TGTTGATCTC	120
	GGTAAATTA ATTCTGC	137

30 (2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

40	ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG	60
	AACAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG	120
45	AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG	180
	ATTTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT	239

(2) INFORMATION FOR SEQ ID NO: 3213:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60  
 5 TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120  
 TCAAAAGTCT TGATATTTGA TACCCACGCT 150

(2) INFORMATION FOR SEQ ID NO: 3214:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

20 CTAAGCATTG GTTTAAACTA ATGTTTCAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT 60  
 nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120  
 TTACGATATT ATTAAACAAC TGTctATCAT TAACGAAAGC AATTAACAAG AGTACTTGTT 180  
 25 GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240  
 TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300  
 TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360  
 30 TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

(2) INFORMATION FOR SEQ ID NO: 3215:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60  
 45 CAGATAATTT AGATAAATAA TTAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120  
 ATAAC TAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180  
 TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTAT GTATGAATGA ACAACTTTTT 240  
 50 GACATCATTA AGAATATAAA TGC GTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA 300  
 ATTTTTCAAT AACAAATTGCG CCACTAAAAC TCAAAATTTT CACCACCAAC ATCCAAATTA 360

55

## (2) INFORMATION FOR SEQ ID NO: 3216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60  
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120  
 CTTGCTTTAT GCTATGGGTT TTTCAAACCTT AAA 153

## (2) INFORMATION FOR SEQ ID NO: 3217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TGTAGACCCA TCAATTGCAG 60  
 CCATTACATA TGCGBAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120  
 AnATAAAATT ATTACATC 138

## (2) INFORMATION FOR SEQ ID NO: 3218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60  
 TTATGCMITT TaTTGCMcMA GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120  
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180  
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTCGATGGG CCAAACACAA 240  
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTTGA TTAAACAAAT TTATATGAAG 300

AACAACGTGA TG TAGGGGTT ATTACAGGTA GTGAGATTTC GAAACAATAT GGAGAAGCAG 420  
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGCAGC 480  
 5 ATATGCA 487

## (2) INFORMATION FOR SEQ ID NO: 3219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60  
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120  
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

## (2) INFORMATION FOR SEQ ID NO: 3220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTGC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCNCGG 60  
 35 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120  
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180  
 40 TATGTAATTG TTTTGTGGTT ACG 203

## (2) INFORMATION FOR SEQ ID NO: 3221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTTCAGA 60

GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180  
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240  
 5 TGAACCACTT ATTGTAAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCCTCA 300  
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCCnGGGG TACACCTGGT CCACTTCATC 360  
 A 361

(2) INFORMATION FOR SEQ ID NO: 3222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60  
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120  
 25 GTGCGTACAA GAATTAATCA AGGTTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60  
 40 AATACATCTC CAACATTTGC CTTnAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120  
 TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCTAAGC ATATTTCTGA 120  
 TGATTTAACA CATTATGAAA CGAGA 145

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60  
 CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120  
 TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60  
 TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120  
 CATCTAnTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CanAAATTCG TCATTCAGTT TCAACTTTAT 60  
 CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120  
 TTATCTGGCA ATAATCGTTG 140

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60  
TGACTTGCTT GATAAATAGC AACAAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

## (2) INFORMATION FOR SEQ ID NO: 3229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60  
ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GntTCTACA 119

## (2) INFORMATION FOR SEQ ID NO: 3230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCCGTAC AAATCTCCAT nAACTAATTG 60  
CTAAATGTTG GAAAAATTC TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCCTACAA 120  
GAGCAGGG 128

## (2) INFORMATION FOR SEQ ID NO: 3231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60  
 AAGTATCGTG TACAAGTTAT GAATGANTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120  
 5 TTC 123

(2) INFORMATION FOR SEQ ID NO: 3232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAAC 60  
 20 CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA TTAGGACATA 120  
 TAAATTCATC ATTAAGTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180  
 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT TTATTAAAAT 240  
 25 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAAATAACC 300  
 GAAGtATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360  
 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420  
 30 TTAAGTTGGC CATTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480  
 GTTTTAGAAA AaCTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540  
 35 CTTTCGGAAT AATCATCAAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTtaCGGG 600  
 TCTGTTTTCT AATTTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660  
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720  
 40 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTTGAAT 780  
 TTTCGTTCAA TTTCGATTCT TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840  
 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900  
 45 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960  
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020  
 50 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080  
 TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140  
 CGCTATCAGG TATCGTTTCA ACAATTTTCA TAACATATCG CGAAATATCA ATTTGAGGAA 1200



GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320  
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380  
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440  
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500  
 ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560  
 10 CTGCTGTTTT TTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTTA ATAATTGAA 1620  
 TATGGrAAAT GTATTaWTct CTCATTTGTA TAGATT 1656

## (2) INFORMATION FOR SEQ ID NO: 3233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

25 TTGCTCATAA ATCTTTTCTT GCGCTCTGA ACACTATCTT CTATTCTGTC GGAATTTTTC 60  
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120  
 30 GGTAAATCCA 130

## (2) INFORMATION FOR SEQ ID NO: 3234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

40 GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCCTGGG 60  
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120  
 45 AA 122

## (2) INFORMATION FOR SEQ ID NO: 3235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAAGT CTACTATTGA 60  
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAAGC ATTACATGCA TGAACCCAGT 120  
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTTG CAGnTTCCAC ATG 173

## (2) INFORMATION FOR SEQ ID NO: 3236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60  
 AGCGATTAnA AAGCATTTAT CAAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120  
 CA 122

## (2) INFORMATION FOR SEQ ID NO: 3237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

35 TTTTTTGCCC AAAATTTTGG GGTTTTTTTT GGGTTAAAGG AAAAAAATT TTAAAGGGG 60  
 GGGGGGGGTC CCCCAAAAT TTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120  
 40 CCCCCCCCCT TTGAAAACC CCTTAAAAA ATTTAAngGT TAAATTGGAA AAAAAAATTT 180  
 AA 182

## (2) INFORMATION FOR SEQ ID NO: 3238:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGAnGTTc GACAACGTAT TGTGGCAGAT GTTGCAGTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60

GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60

AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120

AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60

TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAATAAATA GCGACGGAAT CACACCTTCT 120

GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60  
10 TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120  
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60  
25 GTTGTTATAG TCTAACAATG GTTGGCTCCT CTTAtTTTAT GTGCTAAAAA TTTATAGGCA 120  
ATTTTATTAC AACAAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATT 180  
30 AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60  
45 CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120  
ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180  
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

50 (2) INFORMATION FOR SEQ ID NO: 3245:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

5 GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTTAA AATTTGGAGA TTATGTGTGG 60  
TGTTC AAGTA TGC GTTCaNT AATTGATATT GGCGCACCGT ATAACCATGT CAAAGTA 117

## (2) INFORMATION FOR SEQ ID NO: 3246:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTTG TACA TACGCATGAT 60  
20 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTTGnCC AATTGTTACT ACCGTTC 117

## (2) INFORMATION FOR SEQ ID NO: 3247:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

30 TACACa nCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60  
35 AGCCAACATG ATGCTAGTTT GATTAAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

## (2) INFORMATION FOR SEQ ID NO: 3248:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

45 CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60  
50 ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120  
CnTTTGGTCC TGCCA 135

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTACATG CCATCTGAAT CTCTAATTTT 60  
 AAAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

## (2) INFORMATION FOR SEQ ID NO: 3250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60  
 TCTAGTATTC CAAGTTGAAA AAACTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120  
 GA 122

## (2) INFORMATION FOR SEQ ID NO: 3251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60  
 CAAATTCATC AATCACAATT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120  
 CCAGTACATT AA 132

## (2) INFORMATION FOR SEQ ID NO: 3252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60

5 TGTAAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

## (2) INFORMATION FOR SEQ ID NO: 3253:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTC 60

20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120

GTAACGGCAC TATATTGAAA 140

## (2) INFORMATION FOR SEQ ID NO: 3254:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60

35 TTTCTCTTCT ATTTAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120

CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC ArACGTAGCA 180

40 ATGAAATCAT CTAATTGTGC TTTAACCTWT TCTTGTGTAC CTGcAATGAT GCGTGCTTGg 240

ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300

TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACChA ATAACCAAAC ATCTAAGGCA 360

45 GTTGTAAGCG GChACTTCCG CTTCGTTATC AGChACAAG 399

## (2) INFORMATION FOR SEQ ID NO: 3255:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTTCGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAC 60

GAAGCTATCG TCTCACTAnC CTTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

## (2) INFORMATION FOR SEQ ID NO: 3256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAntTC AGTTAGTAA 60

AAGTCTGTGA GTAAGGGTGT ATGGAACTG GTTAAATATT ATAGAG 106

## (2) INFORMATION FOR SEQ ID NO: 3257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAACCTGT ACATCGTCTA ATAATAAGTT 60

GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

## (2) INFORMATION FOR SEQ ID NO: 3258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60

GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

## (2) INFORMATION FOR SEQ ID NO: 3259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

	GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG	60
10	CACCTTGCAT ACTTTTAAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC	120
	GnTT	124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

25	TACCAATGTA TATCCATATA CTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT	60
	TTTGCTTGAT TAAATCTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG	120
	TACAATAnAT	130

30

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

40	GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCTTAA TTTTTTAATT AAATTTTGA	60
	ATTAAAAAG GAAAAAnTCC AAAGGTTAAT TTAAAAAAA GCCCAAGGTT TTAAAAATTC	120
	CCCCAACCAAA AAAGGGGGGG AAAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG	180
45	GGGCCCTCCC TTGGGGGTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA	240
	ATTGGGGGTT GGGGCCCTGG GGGAAAATTT TTGCCCTTTC CCAAGGGGTT TTTTAAACC	300
50	CGGATTTTTG GAAAAAAAAG AGCCCATTTT CCCCCAACCC CnAAAGCCCA GTTCCCGCCC	360
	ATTTTCCCGG GGTAACCCTG CCCCCACCGG GGCCATTTTT	400

(2) INFORMATION FOR SEQ ID NO: 3262:

55

(A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTGGATGT TGAGAGACGT 60  
GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120  
GCGACGGCTG ATGG 134

15

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25 TTTTTTCTG TTGGTACTTG TTTTGTGGTT GCGATTGTG GTGTGTCTGA nTTAGTAGAT 60  
TGCATTGGTT GTGGCGTGTG TGCTTGATGG AGGTGTTGTC ACTTT 105

30

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40 GTTCCATCAT TCCCACcAT ATCCAACATG TGGGCTACTG CAATGCTTTA GGCGTCAATG 60  
CCTCATCATC ATCAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

45

(2) INFORMATION FOR SEQ ID NO: 3265:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

55

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTGCCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

TTACCTTTAA AATAAnGTTT TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG  
 GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA

60

104

(2) INFORMATION FOR SEQ ID NO: 3267:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACACACAT GCAAATGGTT CAAGTATCAT  
 ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA

60

117

(2) INFORMATION FOR SEQ ID NO: 3268:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC  
 AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C

60

101

(2) INFORMATION FOR SEQ ID NO: 3269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60  
 5 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120  
 ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGGT TTAGCCTGC nGCTGCCTCG 180  
 GGGTTTCTT TAAATTAATG nAACCGC 207

## (2) INFORMATION FOR SEQ ID NO: 3270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

ATATTCGCAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTAC AGTGATAAAA 60  
 GGGCTTGGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

## (2) INFORMATION FOR SEQ ID NO: 3271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60  
 GATCAGCACC AGATATTGCA GGTA AAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120  
 TT 122

## (2) INFORMATION FOR SEQ ID NO: 3272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

GAAGGATGAT GATTCCGAGC AnCTTCTTGC AGAAGAnGCG GnAATAACGT GACATATTGT 60

TGCGAGCGCT TGACAATCTA TTCTTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180  
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTGGA TTTTtTGAAA ATAAAGCAGT 240  
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300  
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTTACTT TGTACATTAT TGTAATTTCA 60  
 GTAATACGAG GCAATGTCAG TnGCAGTGT TAATAAATTT TGTTGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60  
 TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAActGGT AAGCCATTAC 120  
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180  
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240  
 nTGATGTCGC AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300  
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

45 (2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60  
 CCGGCGATAT CTGGCATCTT TTATTTCCGC ATTTTTTCAA ATCATGGTTA TTCCAGTTTG 120  
 5 GCGGCTTAAA AATTChTT 138

## (2) INFORMATION FOR SEQ ID NO: 3276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GnATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60  
 20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

## (2) INFORMATION FOR SEQ ID NO: 3277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTTATC GTGTGGCAIT 60  
 35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACCTGTT GCGAGTATTT CCGGTCTCGT 120  
 CATT 124

## (2) INFORMATION FOR SEQ ID NO: 3278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60  
 50 CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

## (2) INFORMATION FOR SEQ ID NO: 3279:

(A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60  
GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60  
TTCGTTCCCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

40 ACTATGTTTG AaAAATTCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60  
ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

55 ACTTGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

## (2) INFORMATION FOR SEQ ID NO: 3283:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

AAATGACGAT AGAGTCAGGT ATTAATCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60  
 TTATGTTGAA GGCATCTTT TGGCGTTACC GGGTTGGGCA 100

## (2) INFORMATION FOR SEQ ID NO: 3284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

TTAAGAAACC GAGCAGCGCA TAAncCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60  
 CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

## (2) INFORMATION FOR SEQ ID NO: 3285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

TAAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAAC GGCTGTTTTTA 60  
 AAGCATCCTC CCATAAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

## (2) INFORMATION FOR SEQ ID NO: 3286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 95 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60  
 5 TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

## (2) INFORMATION FOR SEQ ID NO: 3287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60  
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCnAG AACCCATTTT TTGAATATTT 120  
 CACCACTCGA ATCATCAATA C 141

## (2) INFORMATION FOR SEQ ID NO: 3288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60  
 35 GCGGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

## (2) INFORMATION FOR SEQ ID NO: 3289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60  
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

## (2) INFORMATION FOR SEQ ID NO: 3290:

- (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTTT AAGCGATGAT TGCAATTAGA 60  
 CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

## (2) INFORMATION FOR SEQ ID NO: 3291:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTGA ATTTAATTGA TTTTATATT GGAGATGGTT AAAATGCTAA 60  
 AACTCAACAT GAGTAACCAA AATATTGCCC TTA AAAATGC TGATCATTG 109

## (2) INFORMATION FOR SEQ ID NO: 3292:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60  
 40 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120  
 A 121

## (2) INFORMATION FOR SEQ ID NO: 3293:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

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GCGCGTAATA CCTGCAGTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

(2) INFORMATION FOR SEQ ID NO: 3294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT 60  
 AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n 111

(2) INFORMATION FOR SEQ ID NO: 3295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTTGTCCG AATCCCCATC CTGCACCTGA 60  
 TAATAAGGCG AATAGCAAGT TGGTTCCCGT nGGGAAGCCA CTGA 105

(2) INFORMATION FOR SEQ ID NO: 3296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

ATTTATTCAA AACCGCCAC ATGGGGCAAC GGTGCCATG GCATGATAGT CCAGATACAT 60  
 GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTA AAAACCT GCGGGTTGGT TAAACCATTT 120  
 AACCTAAATG GGTTC AAGG GTTAACGCGG TTTAAATGTT TGGAAAGGTT TnCCCAGTTT 180  
 CCAAAAAGTT TTTnATTCCC C 201

(2) INFORMATION FOR SEQ ID NO: 3297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTCCTGA 60  
10 GAAATATTTT CATTCTTTAC ATTTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA 120  
TCTTGTAATT CTCTTGAAAC ATCATAATC TkGGCCACAT TTTCAGCACC TkGAATCATT 180  
GATGGGTCGC TCATTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT 240  
15 TCGTACACAG AATGCGGTCG TTTGATTTTC CAAGGTGCTC GACTTGTACT TTCAACACCA 300  
CCTGCAATAT ATACCTTGCC AGCTCCGGCT TGGATCATGC GACATGCATA TTGaACACTT 360  
TCAAGTCCAG ACCCACATTG cCGATCGrTT GTGaCGCCAG TATTGAAGCT TAAGC 415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

30

TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTG 60  
CCATTTAGGT GCATCGACCA ACTGCCCCGAC GAAAAGCCAT TTTGAAAACC AGAANGATGC 120  
35 CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG 164

(2) INFORMATION FOR SEQ ID NO: 3299:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

45

GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTITT TAAATGCGAT GTGTGGCTTC 60  
TACATAACGG GAAATTTTAA GTTTTATGAA TCnACATATC AATTGC 106

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(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCANTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60

10 CATTTAAGGA AGCGATTAC AATCGAGAAC ACAAAGTACA AC 102

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAATT GATATTGGCG 60

25 CACCGTATAA CCATGTCAAA GTACCATTG NAATCAGTCA TTGGCGCATT GGCTGCCCTA 120

CGGTTCA 127

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTTGAAACGT CCATGGACCC AATTGATTAA 60

40 TTGGnTGTA CTCGGTCAAT GGTATATCC TAAATGCACT GGCCTGCTGG TGTCTTCTG 120

GGCGTTGCTT CGGAAAT 137

(2) INFORMATION FOR SEQ ID NO: 3303:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120  
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180  
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240  
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATTATT 300  
 TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTCGGTT 360  
 10 AAAAGCGTTG GCACAATCCA CAATGCGAAC TGCCAAAGT 399

## (2) INFORMATION FOR SEQ ID NO: 3304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:  
 CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60  
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

## (2) INFORMATION FOR SEQ ID NO: 3305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:  
 TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTACCCA TTTTGTAAA TGGAACATGG 60  
 AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTTGCCTA TTCATTCCAG 120  
 40 CTTTGTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180  
 TTATGTCCAG TTGGACGCCA GA 202

## (2) INFORMATION FOR SEQ ID NO: 3306:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60  
 AACTACTCCC G<sub>n</sub>CAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120  
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTTCTGTTA CCTGCGCCTT CTTTTGCGG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60  
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60  
 35 ATGGTTCGCA ATAATTTTAA AATACCTTCC GCTACATTG ATTTAAAGCT GGTTGCGCAn 120  
 TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCCTTTTA TCGTAGTTGG TGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60  
 50 GGAnACGGAC ATTCAAAAGG GATTTAGTTC ATCCCAGATG GATTTCATT TGGGGAATTC 120  
 CATTTGGA 128

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCACCTACGA CATCTGTAGC TGGTATTGAT 60  
 CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60  
 CAGCGATTTC GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60  
 AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120  
 TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60  
GCACAGTTAA ATGATGCCAA AG 82

(2) INFORMATION FOR SEQ ID NO: 3314:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60  
TTATCAAAAT AGTGAGGGGC GTCATCA 87

(2) INFORMATION FOR SEQ ID NO: 3315:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCATTT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60  
TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120  
TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGTnTA TTAGCAACTT GGAAGTGCCA 60  
TTGTTAATTT CAGCTGTCTG TTACATTTCA ACCATAGTCT TTCACAAT 108

(2) INFORMATION FOR SEQ ID NO: 3317:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

10

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT	60
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA	120
AAGATGATGC ATTAAATGCA CG	142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

25

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT	60
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA	120
AGAGCGAGTG ACTTAGGTCA AACACAGAG CAAGGCGAAT GGAAGCCAGT TATTCATGAT	180
GCAATCAGCG ATAGTTTGTAGT AGTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT	240
AAGAAGTGGA ACTTAAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA	300
ATGACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA	360
GATGGGATAT CATCGTCCAA TCCnAC	386

35

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

50

ACAATGAATG ACATGATTG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA	60
ATCGCCGGTC ATAATGTTTC TTGnCCAATT AACTCAATAT TCtTCATGAC ATTTTCAAAT	120
GGC	123

(2) INFORMATION FOR SEQ ID NO: 3320:

55

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

10 GGCGAACTGT CAATTGCCGG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGT 60  
 AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

25 GCGCCGGTTT TAACAGGTAA TTTAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60  
 AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

30

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 87 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

40 TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60  
 TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

55 TGCCAAATGT TCCATAATT TCATTACGAN TCTTAAGTAG GTGGCTATCA TTACGATGCC 60

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCACTAAAA TAATAGTTGA 180  
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240  
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300  
 TAGTGCCAAA CGTTGTTTCA TACCCCGGA cAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360  
 TTCTAAATCA ACTAATTAA GCTGTGCGTT AATCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3324:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGhATCC TAATGTATTT 60  
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25 (2) INFORMATION FOR SEQ ID NO: 3325:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

TCTGAANTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60  
 TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40 (2) INFORMATION FOR SEQ ID NO: 3326:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

50 TGTCACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60  
 TAGCCTTCTT CATTAACC 78

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCAATT 60  
ATATTCACTA TCCATTAGAC CAAATGGGCC ATTCCAATA ATCCCGCGGT GGTTTCCGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60  
CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60  
TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

## (2) INFORMATION FOR SEQ ID NO: 3331:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

GGACACTAAC ATTAATATGG ACTGGAATG TTGCTGTAA TAAACTCATA CCAAATCCTG  
GGCATCTCTT

## (2) INFORMATION FOR SEQ ID NO: 3332:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

CCTTGGGCAC CTTCAATTG CATATTACGA CGTTTTGCAG CTTGGTTCAA TTGGCAATAA  
CTACACCTAG TGCAGTTGGA TC

## (2) INFORMATION FOR SEQ ID NO: 3333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA  
AAAACAAGTA TATTGA

## (2) INFORMATION FOR SEQ ID NO: 3334:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

5 TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTTCCTGGC 60

ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60

20 CATACGAGTA AGGG 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60

35 CATAGGAGAA AACAGG 76

(2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTTA CTAATAAATG TATTTAAATA 60

AGTAGTACCT AA 72

50 (2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTAAATATGC 60

10

TGTCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

25

TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTAAATGAAT GTCTTCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

40

ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTAAATCCTT GGTGCTCTT TATTTTATTT AAATTGTAGA 60

55

ACCTAGA 67



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAG CACGTTTTAC AAGCATCAAT CCATTAATTA ATAATTCCAT TAAATGTAGA 60  
 TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 415 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TGCGGATATC 60  
 ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGAAATGA 120  
 AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180  
 AAGTGTA<sub>CGG</sub> TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240  
 CATGCTTTGT CTGGGATATG AAATGATTGA CGACAAGGG TGCCATTGCA ACAAATGAAG 300  
 TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360  
 CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60  
 TCGCAGTGGT AATTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

(A) LENGTH: 474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10 CGGGAGGTGT TAAntCTTCA CAAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60  
 TCGGTTTCAGG TGCCACAGGA AGTGATTCAG GTAGCnAAGG GTTATCTGAT ATTTTGAAAC 120  
 CTGCATTAAG TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180  
 15 ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC 240  
 CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTCG CGAAAAATTC GAAGAACACC 300  
 ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360  
 20 TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420  
 TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAACTGG AGAACGAATT TCTG 474

25 (2) INFORMATION FOR SEQ ID NO: 3346:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35 AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60  
 TTAG 64

(2) INFORMATION FOR SEQ ID NO: 3347:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50 AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAAACAAT 60  
 GTTTTAAGTT GTTGATTAA AATATTAAT 89

(2) INFORMATION FOR SEQ ID NO: 3348:

55

(A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10 ATAACCTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTTCTTT 60  
 AAAGAACAAT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT 107

(2) INFORMATION FOR SEQ ID NO: 3349:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25 CAACGCATCC TGCACCTTTTA CCTATTCCTG AATCACCGGT AATTAGTACA CCAACACCGT 60  
 AAACATCTAC TAAA 74

(2) INFORMATION FOR SEQ ID NO: 3350:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40 AGATGCACCT ACTTCTAACT GTCGCAACA TCGCCGAAT CATTTCAAAA CTACGTTCTG 60  
 TA 62

(2) INFORMATION FOR SEQ ID NO: 3351:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55 GCTGCAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT 60

(2) INFORMATION FOR SEQ ID NO: 3352:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTTCGAT ATAGAACATC TAGCGACGTC GATTCGCAAG GTTGAACCAT 60  
 CTACATTAGG TGAGGAA 77

(2) INFORMATION FOR SEQ ID NO: 3353:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

(2) INFORMATION FOR SEQ ID NO: 3354:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

(2) INFORMATION FOR SEQ ID NO: 3355:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATACC TTTAGGGTTA CTACCAGCT TAGGTAGTGC ATAACCTTTA ACCACATCT 59

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAT GCTAATAAT CCGCCGAACA ACATGCCGTT GTTTGTGA 59

(2) INFORMATION FOR SEQ ID NO: 3357:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCACGCCCTT TGAATATGGG AACTCAAAC GATCTACTGG CTGATGTAAT 60

TACCCCTGTT TTGATTG 77

(2) INFORMATION FOR SEQ ID NO: 3358:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA 59

(2) INFORMATION FOR SEQ ID NO: 3359:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA 59

(2) INFORMATION FOR SEQ ID NO: 3360:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25

GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTCGCT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50 CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTTAA TCGGTTGATT AAAAGTGGCA AAGCACGTGC ACATACGA

58

10

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

20

GTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT

58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTACTTT GTAATTCAG TAACAGTTGA TCATCATG

58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

45

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC

58

(2) INFORMATION FOR SEQ ID NO: 3368:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA 58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG 58

(2) INFORMATION FOR SEQ ID NO: 3370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA 60

TTGACGGC 68

(2) INFORMATION FOR SEQ ID NO: 3371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

ATTACCAACA GCGAAAATAT TGAAAAGCTG TAAAAAAGCT GGTGCAsmCm TACTTGGATT 60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT 120

TGCACTTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG 180

CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA kCACTTTTAA CGACCAGTTA 240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT 300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA 360



## (2) INFORMATION FOR SEQ ID NO: 3372:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTCAACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA 58

## (2) INFORMATION FOR SEQ ID NO: 3373:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG 57

## (2) INFORMATION FOR SEQ ID NO: 3374:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATTT CTTCGTG 57

## (2) INFORMATION FOR SEQ ID NO: 3375:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA 60  
ACTAACAGAC 70

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG

(2) INFORMATION FOR SEQ ID NO: 3377:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG  
 CTCGCATCCA

(2) INFORMATION FOR SEQ ID NO: 3378:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT

(2) INFORMATION FOR SEQ ID NO: 3379:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC

(2) INFORMATION FOR SEQ ID NO: 3380:

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10

ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG

57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT

56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35

GAACACACAG GCAACCCAAA GCAGTGACGG CGAAAnTTGG ATTGATCTTG CAGCATTGAA

60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT

105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

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nGTATGTGAA AACTATTTGG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG

60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC

106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

TAGAG 65

25

(2) INFORMATION FOR SEQ ID NO: 3386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTAAAT TATTTCTATT TGCTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

TCTTAACTGC A 71

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(2) INFORMATION FOR SEQ ID NO: 3387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

10 TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCTACTTT TGTTCG 56

(2) INFORMATION FOR SEQ ID NO: 3389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

20 ATTTATTAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

35 AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

50 CAAACGCAAT AGCTGGTGAC TTAAGTGGG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTTATTAC AAAAGCCAAC TGTAT

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10

(2) INFORMATION FOR SEQ ID NO: 3393:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTG

55

(2) INFORMATION FOR SEQ ID NO: 3394:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC

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35

(2) INFORMATION FOR SEQ ID NO: 3395:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCATT TGTTGGTACA GGTATGGAA CACGTTGCAG CACGTGATTC TGGTGCGG

58

(2) INFORMATION FOR SEQ ID NO: 3396:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

(2) INFORMATION FOR SEQ ID NO: 3397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

(2) INFORMATION FOR SEQ ID NO: 3399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

## (2) INFORMATION FOR SEQ ID NO: 3401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG

55

## (2) INFORMATION FOR SEQ ID NO: 3402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG

54

## (2) INFORMATION FOR SEQ ID NO: 3403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT

58

## (2) INFORMATION FOR SEQ ID NO: 3404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAAGT TATCTAGCGC TATTGTTCTT

60

TGCTCT

65



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:  
 AAATTTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC

(2) INFORMATION FOR SEQ ID NO: 3406:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:  
 TCGATTTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC

(2) INFORMATION FOR SEQ ID NO: 3407:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:  
 AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT  
 TAAAGATTAG AAGG

(2) INFORMATION FOR SEQ ID NO: 3408:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:  
 TGATTTTACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT  
 AGTGCTCA

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

(2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

(2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

(2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA

TCA

(2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10 ACTACCATTG CTTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC 53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC 60

TT 62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCATATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG 55

(2) INFORMATION FOR SEQ ID NO: 3416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG 53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA

59

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(2) INFORMATION FOR SEQ ID NO: 3418:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20

CGTGGTCACC ATCACCAATT GCTCGATCTA ATTCAGTAAT TCAGATTCAT GTT

53

(2) INFORMATION FOR SEQ ID NO: 3419:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT

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35

(2) INFORMATION FOR SEQ ID NO: 3420:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45

TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG

53

(2) INFORMATION FOR SEQ ID NO: 3421:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATAA TTAAAACTTA GACCATTAC 60  
 5 CCCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTTAAG TCGCAATAGT AGCGGCCGTT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

(2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTCGCAG ACTAGTTTAG GGTCAAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

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52

(2) INFORMATION FOR SEQ ID NO: 3427:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTATGTTT ATGTGAATGC TTGCTTGCTG GACTGTCTT TT

25

52

(2) INFORMATION FOR SEQ ID NO: 3428:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

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52

(2) INFORMATION FOR SEQ ID NO: 3429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTG TGAAAAAGGT ATTATGGCGG CA

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52

55

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTCTTTTTT TTATAAAAAT CTTATGCTTT 60

TTAACTAATT GTAAGA 76

## (2) INFORMATION FOR SEQ ID NO: 3431:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGGTAAGTC GTATTAGAAC TAAAGCGGCT 60

## (2) INFORMATION FOR SEQ ID NO: 3432:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

## (2) INFORMATION FOR SEQ ID NO: 3433:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTAAATTT 60

TAAATTTT 69

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:

GATCGCTATC CATTAGCTAA ATTTAAACGT TCAAACCTCAG GTACATGTTA C

(2) INFORMATION FOR SEQ ID NO: 3435:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:

TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

(2) INFORMATION FOR SEQ ID NO: 3436:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:

ATTAAAGCCA ACATTAATTT ATCCACTATT AACAAATAACG GCTACAGGCT TATTAATGAT

TTATACCTTT

(2) INFORMATION FOR SEQ ID NO: 3437:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:

TTTGTTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTCTTAG A

(2) INFORMATION FOR SEQ ID NO: 3438:



- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10 GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G 51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A 51

(2) INFORMATION FOR SEQ ID NO: 3440:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35 CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA 55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAAACCAG TGTGTAAAAC CGGAACTACT 60

50

ATGAGGGGCA TGAAAGT 77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCCGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA

55

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(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACTTTG GGATAAAGGT GATGCCCAAA CTTTCCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

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ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC

50

(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

50

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTCCTCA TCTCTCTACT

60

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

TTATCACGGT ATATGAGGGG ATTTGAGG

88

(2) INFORMATION FOR SEQ ID NO: 3451:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

(2) INFORMATION FOR SEQ ID NO: 3452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GCGTGATT ATCAAGTTTG

60

GGTA

64

(2) INFORMATION FOR SEQ ID NO: 3453:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

AAGAATAAGT A

131

(2) INFORMATION FOR SEQ ID NO: 3454:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGGA AGAAGCGCAN

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

## (2) INFORMATION FOR SEQ ID NO: 3459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC

50

## (2) INFORMATION FOR SEQ ID NO: 3460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG  
CAAAAGCT

60

68

## (2) INFORMATION FOR SEQ ID NO: 3461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

51

## (2) INFORMATION FOR SEQ ID NO: 3462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

56

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:  
 ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT 50

(2) INFORMATION FOR SEQ ID NO: 3464:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:  
 TCITTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT 50

(2) INFORMATION FOR SEQ ID NO: 3465:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:  
 AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTCG CCCGACA 57

(2) INFORMATION FOR SEQ ID NO: 3466:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:  
 ACATCCGAAA GATGACTTGT TTAaaaaAGC AGAGCATGAT TTGCTTACTA TGATTACAG 60  
 CGG 63

(2) INFORMATION FOR SEQ ID NO: 3467:

55

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCTTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25 (2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

50 CCTGTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

5 TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT 50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT 54

(2) INFORMATION FOR SEQ ID NO: 3473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

30 TAATAGGCAT TCCATTAGG TCGTCGACA ACTGCAACGC AAGCATTGGA AACAGA 56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA 55

45 (2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GCGAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAAnCATTcG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CCGTACACAC GCTTTAGATT TAACGTTATG

50

(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTcAG CTGCTAACGA GTTCCTGTTA CTGTTcATGT CTATCACTTT GCGTTCCCTC

60

## (2) INFORMATION FOR SEQ ID NO: 3480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC

50

## (2) INFORMATION FOR SEQ ID NO: 3481:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTCTGT TGTAGAACAA

60

GA

62

## (2) INFORMATION FOR SEQ ID NO: 3482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T

51

## (2) INFORMATION FOR SEQ ID NO: 3483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT

54

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG

(2) INFORMATION FOR SEQ ID NO: 3485:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG

(2) INFORMATION FOR SEQ ID NO: 3486:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG

(2) INFORMATION FOR SEQ ID NO: 3487:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTGTGAT CACACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT  
 AATGTAA

(2) INFORMATION FOR SEQ ID NO: 3488:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10

TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTG CCACCTTCAC CACTATATTT TCCCATGGTC

60

(2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

35

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC

50

(2) INFORMATION FOR SEQ ID NO: 3491:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT

52

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACCTCTTC TAATGGGATA ATCTCTTCAT GT

52

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACC GGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG

56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AACACGTA

59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT

55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

AnTGTAACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA

50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

## (2) INFORMATION FOR SEQ ID NO: 3501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC

52

## (2) INFORMATION FOR SEQ ID NO: 3502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT

50

## (2) INFORMATION FOR SEQ ID NO: 3503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCGACTT GGC GGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC

50

## (2) INFORMATION FOR SEQ ID NO: 3504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA

60

TCGC

64



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA

(2) INFORMATION FOR SEQ ID NO: 3506:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTAAAA T

(2) INFORMATION FOR SEQ ID NO: 3507:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT  
 TTAA

(2) INFORMATION FOR SEQ ID NO: 3508:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT

(2) INFORMATION FOR SEQ ID NO: 3509:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

CAGATGCAAA TTGACATGGT CATCAACATC nGTnCATTA AAGATGGACG

50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTGATTCC CACCGCCACA TCATGATATT TATTCATAGA

60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG

94

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT AACTGAAAA ATGGGTAATG GTGCAAACAT AGTA

54

(2) INFORMATION FOR SEQ ID NO: 3512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn

50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC

58

10

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20

GTGTTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC

60

AATCTG

66

25

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35

ATGCCACTGA TAATGChnCT GAACTTATTG ATGACTTCTC ATTAGACTAT

50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC

50

50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTT C 50

20 (2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35 (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50 (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60  
GTGATTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGA 57

20 (2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

TGGTGGAGGT TTTGTTTTTT CCGTGTCGGT TTTTGTTTTT GTCTTGTTTT CTTTGTTTTT 60  
TGTGTTCTCT TT 72

35 (2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

5 TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC 59

(2) INFORMATION FOR SEQ ID NO: 3526:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGTACA 50

(2) INFORMATION FOR SEQ ID NO: 3527:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

30 TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT TGTATGCAGGC CT 52

(2) INFORMATION FOR SEQ ID NO: 3528:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAAAA 50

45 (2) INFORMATION FOR SEQ ID NO: 3529:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

5 (2) INFORMATION FOR SEQ ID NO: 3530:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

30 GAATGCAAAA TCCATTTGTA AGGAnATCGA ATGGTTTAGT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

55

## (2) INFORMATION FOR SEQ ID NO: 3534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGTCCTA GTTTAATTTA CGAGTGGCGT AA 52

## (2) INFORMATION FOR SEQ ID NO: 3535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60  
 CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120  
 ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180  
 CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTTGTACAT GTTCGTGATG 240  
 TAGATGGTGA AAAAAGTGA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAACAA 300  
 TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360  
 TGCTTGACA ACCTTCTTAT TTCCCAATTC CAGAGGTTAT 400

## (2) INFORMATION FOR SEQ ID NO: 3536:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60  
 GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120  
 AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180



## EP 0 786 519 A2

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300  
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360  
 5 CGTTTTTCATT ATTTTAAATG CTCATTTACA TAAGTAACT CTGCTTTAAA ATAATTJAAC 420  
 TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGA 480  
 GTGTTCCTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAATCTTTA 540  
 10 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600  
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCATT 660  
 15 TACAAAAGTA AACTCCGCTT TAATTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720  
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 780  
 ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840  
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900  
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960  
 TTACTCCACC GGCTTCGGGT GTTACAACT CTCGTGGTGT GACGGGcGGT GTGTACAAGA 1020  
 25 CCCGGGaACG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGtTCC AGCTTCATGT 1080  
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

## (2) INFORMATION FOR SEQ ID NO: 3537:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

40 GGGGATCCCC AGCCAGAAGA TTTATTTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60  
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAaGTTG AAACATCAAC ATTAGGTGAA 120  
 45 GAAAGTGAAG ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180  
 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240  
 TTACCATTCTG TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300  
 50 ATTTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360  
 TATCTAAGAT ACTGGCGAnG ATTGTACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420  
 ACCC 424

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG	TTAAAAGGTA	AACAAGGTCG	TTTCCGTCAA	AACTTACTTG	GTAAACGTGT	60
TGACTATTCA	GGACGTTTCAG	TTATTGCAGT	AGGTCCAAGC	TTGAAAATGT	ACCAATGTGG	120
TTTACCAAAA	GAAATGGCAC	TTGAACTATT	TAAACCATTC	GTAATGAAAG	AATTAGTTCA	180
ACGTGAAATT	GCAACTAACA	TTAAAAATGC	GAAGAGTAAA	ATCGAACGTA	TGGATGATGA	240
AGTTTGGGAC	GTATTGGAAG	AAGTAATTAG	AGAACATCCT	GTATTACTTA	ACCGTGCACC	300
AACACTTCAT	AGACTTGGTA	TTCAAGCATT	TGAACCAACT	TTAGTTGAAA	GGTCGTGCGA	360
TTCGTCTACA	TCCACTTGTA	ACAACAGCTT	ATAACGCTGA			400

(2) INFORMATION FOR SEQ ID NO: 3539:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG	TTATTTTGTG	TGGTGACTAT	AGCAAGGAGG	TCACACCTGT	TCCCATGCCG	60
AACACAGAAG	TTAAGCTCCT	TAGCGTCGAT	GGTAGTCGAA	CTTACGTTCC	GCTAGAGTAG	120
AACGTTGCCA	GGCAAATGAC	AAATCGGAGA	ATTAGCTCAG	CTGGGAGAGC	ATCTGCCTTA	180
CAAGCAGAGG	GTCGGCGGTT	CGAACCCGTC	ATTCTCCACC	ATTTATTCTT	AGATATAGCC	240
GGCCTAGCTC	AATTGGTAGA	GCAACTGACT	TGTAATCAGT	AGGTTGGGGG	TTCAAGTCCT	300
CTGGCCGGCA	CCATCTTTTG	AGCCATTAGC	TCAGCTGGTA	GAGCATCTGA	CTTTTAATCA	360
GAGGGTCAGA	GGTTCGAATC	CTCTATGGCT	CATTACGATT	TAATTTTAT	ATTTAGCAAA	420
ATAATGCAGA	AGTAGTTCAG	CGGTAGAATA	CAACCTTGCC	AAGGTTGGGG	TCGCGGGTTC	480
GAATCCCGTC	TTCTGCTCCA	TTATTTTGCC	GGGGTGGCGG	AACTGGCAGA	CGCACAGGAC	540
TTAAAATCCT	GCGGTGAGAG	ATCACCGTAC	CGGTTGATT	CCGGTCCTCG	GCACCATTTT	600
AGCGCCCGTA	GCTCAATTGG	ATAGAGCGTT	TGACTACGGA	TCAAGAGGTT	ATGGGTTCGA	660

GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780  
TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840  
5 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900  
CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960  
10 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG 1020  
GATGAACGCT GCGGCGGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080  
TCTCTGaTGT TAGCGGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140  
15 GaTAACCTCG GGaAACCGGA GCTAATACCG G 1171

## (2) INFORMATION FOR SEQ ID NO: 3540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60  
CTTAACGAGT ACCGGATTG CTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120  
30 GCACGCTTCG CCTATCCTAC TCGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180  
GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCCGCCT CAGCTTAGGA CCCGACTAAC 240  
35 CCAGAGCGGA CGAGCCTTCC TCTGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300  
GTCTTTGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360  
TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCrC ACAGCTTCGG 420  
40 TaATATGTTT AGCCCCGTA CATTTTCGGC GCaGTGCAC TCGACTAGTG AGCTATTACG 480  
CACTCTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGnAC 540  
ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGnTTCC 600  
45 C 601

## (2) INFORMATION FOR SEQ ID NO: 3541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GChAGGACCT TnCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCChC 60  
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT 120  
 TAAGTCCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC ATCATTAAGT TGGGCACTCT 180  
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240  
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300  
 nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360  
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420  
 TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480  
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540  
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600  
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTGT TCATTCAAAT 660  
 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720  
 25 CGAGTCCACT TAGGCCACC ATTAATTTAA TACCTATTG GGGGCTTAGC TCAGCTGGGA 780  
 GAGCGCCTGC TTTGCACGCA GGAGGTCAGC GGTTTCGATCC CGCTAGTCTC CACCATTATT 840  
 30 TGTACATTGA AACTAGATA AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900  
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960  
 CTCACAAGAT TAATAACGCG TTTAAATCTT TTTATAAAAG AACGTAACCT CATGTTAACG 1020  
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080  
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140  
 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200  
 40 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGAG AACTGAAACA TCTTAGTACC 1260  
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

## (2) INFORMATION FOR SEQ ID NO: 3542:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:

CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120  
 CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180  
 5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240  
 GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300  
 ACTTTTAATC AGAGGGTCAG AGGTTCGAAT CCTCTATGGC TCATTACGAT TTAATTTTAA 360  
 10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3543:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 804 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAAATAAC AGTTAATTAT ACCGGTGGTC GGGGTCGAAC 60  
 25 CGCACTCCAC AAGTGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120  
 CTTAATGGTA AACAAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180  
 CACCTATACC TCGTTCGGG aAGGAActGg TtTAAAAGT TGAActACTC CCGCAAATAT 240  
 30 TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300  
 CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360  
 35 CCTATACCTC GTTCCGGGAA GGackTGTTt CTAAAAGTTG AACTACTCCC GCATAAACCT 420  
 GGAGGCGGCA ACCGGATTTG AACCGGTGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480  
 TGGCTATGCg CcAATAACTG GGCTAGCTGG ATTCGAACCA ACGAGTGACG GATmAAAGTC 540  
 40 CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600  
 CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660  
 GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720  
 45 TGCCCCCTATT aAAAAATaATA ATkGGAGGGG GGCAGATTcG AAnTGCCGAA CCCGAAGGAG 780  
 CGGGATTTAC ATTCCGCCGG GTTT 804

## (2) INFORMATION FOR SEQ ID NO: 3544:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTAATCGT TTGAAGTATA 60  
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120  
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180  
 10 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240  
 CATCGCATAA GTTTGATkAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300  
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360  
 15 GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3545:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60  
 30 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120  
 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180  
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240  
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCTTTT CGAACACGGA CCTTATCACC 300  
 CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTTCGGAG TTTGTCTGAA TTCGGTAACC 360  
 CGAGAGGGGC cCCTCGTCCA AAcAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420  
 40 CCCTAAAGCT AATTTCGGAGA GAACCAAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

## (2) INFORMATION FOR SEQ ID NO: 3546:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

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GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120  
 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180  
 5 GCTTTAATCT CTAAAGTCAT GGTAAATCTT GACGACTTAC CATTCGTTCA CAGTGACATG 240  
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GCGCCTTTGn GCGACACGGG 300  
 TAAAAAAGC AGGCGAGTTC TATACACCAC AACAAGTATC TAAGATACTG GCGAGATTGT 360  
 10 CACAGACGGT AAAGATAA<sub>n</sub>T ACGTCACGTG TATGACCCAA 400

## (2) INFORMATION FOR SEQ ID NO: 3547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTTGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60  
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT CGCATCCATT TTTGCCTGG 120  
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTTCTTGA 180  
 CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTGGGCTCT CGCTTACTCA TTTAGCTCTA 240  
 30 CTAAACTCGT TGCGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC 300  
 CATTTTTCTT TGTTGTTGCT TTTTATTTTG ACGTTTTTGA CATAAAAAAA AGAGACCTTG 360  
 35 CGGTCTCAAT GCGGCTCATC GCATCCAnTT TTTGCCTGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60  
 50 GTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120  
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180  
 GTGTTGGCTT ATTACCGAGT GCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTTAC GTGATACAGA 360  
TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60  
AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA TTCCAGCTTC 120  
ATGTAGTCGA GTTGCAGACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180  
CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240  
GGGGCATGAT GATTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300  
AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360  
CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60  
TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120  
TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180  
TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240  
AGGGTGATCG GCCCACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300  
GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360  
TCGGATCGTA AAACCTCTGT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:



(A) LENGTH: 506 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

10	ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA	60
	ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTAT	120
	TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TCGAGCGCT TGACAATCTA	180
15	TTCTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC	240
	TTTTGTAAAT GAGCATTGTA TTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA	300
	AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAAATAT AGATTTTACC AAGCAAAACC	360
20	GAGTGAATAA AGAGTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTCGAAA	420
	GAACACTCAC AAGATTAATA ACGCGTTTAA ATCTTTTTAT AAAAGaAAC GTTTAGCAGA	480
25	CAATGAGTTA AATTATTTTA AAGCAG	506

## (2) INFORMATION FOR SEQ ID NO: 3552:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

	AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTGAT ATTCCTGTAC CACCTATAAT	60
	CGTTTAAATC GATGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA	120
40	AGCAGTAAGG CTGAGTATTA GGCAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA	180
	GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA	240
45	AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC	300
	GAGCGAACTC TCGTTAAGGA ACTCGGCAAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC	360
	TCTTTAGGGT TAACGCCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA	420
50	AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG	480
	GAAGGTAAAG AGGAGTGGTT AGCTTCTGCG AAcTAcGaAT CGAAGCCCCA GTAAACGGCG	540
	GCCGTAAC TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA	600

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	GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT	720
5	GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT	780
	AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC	840
	ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA	900
10	AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATTG ATAGAGTGTA	960
	AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGAAGT	1020
	AGTGATCCGG TGGTTCCGCA TGAAGGGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG	1080
15	ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGCA CCTCGATGTC	1140
	GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCT CCCATTAAAG	1200
	CGGTACmGg CTGGGTTTCA AACGTCGTGA GaCAGTTCCG TCCCTATCCG TCGTGGGCGT	1260
20	AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG	1320
	TACCAGTTGT CGTGCCAACG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA	1380
	AACATnCTnA AGCATGAAGC CCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC	1440
25	CCTCAAAGAT GATGAGGTTA ATAGGTTTCA GGTGGAAGCA TGGTGACATG TgGGAGCTGA	1500
	CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA	1560
30	CTTACTATCT AGTTTTGAAT GTATAAATTA CATTATATG TCTGGTGAAT ATAGCAAGGA	1620
	GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG	1680
	AACCTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTTGTTAA	1740
35	AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT	1800
	AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT	1860
	TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT	1920
40	CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA	1980
	CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG	2040
	AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA	2100
45	CCGGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA	2160
	GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA	2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 518 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60  
 AATAAGCTTG AATTCATAAG AAATAATCGC TAgtTGTTCTGA AAGAACACTC ACAAGATTAA 120  
 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180  
 10 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240  
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300  
 15 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360  
 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGAAGAGGCC 420  
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGaCACTCT ATACGGAGTT ACaAAGGmCG 480  
 20 ACATTgGACG AaTCATCTGG gAAAGwTGaT CCAAGGAA 518

## (2) INFORMATION FOR SEQ ID NO: 3554:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60  
 CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120  
 35 TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGGCAT GGAACAGGT GTGACCTCCT 180  
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240  
 40 AGTGATTTTG CTTCGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360  
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420  
 45 CACTTatCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480  
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAAA TTTCTACGC 540  
 CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCAGA 587

## (2) INFORMATION FOR SEQ ID NO: 3555:

## (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

	GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT	60
10	GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG	120
	CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT	180
	GAGTCGGAAT CACTGTCCGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT	240
15	GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG	300
	CTATCTGGAA TCTGGAGTCA CTGTCCGaaT CTGAGTCACT GGTCTGGAGT CAGAATCGCT	360
20	ATCTGGAATC CGAnGTCATG GTCTGAGTCG GGaATCGCT	399

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

	ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGCCT	60
	ACAACCCCAA CAAGCAAGCT TGTGTTTGT GGCTCTTCCC GTTTCGCTCG CCGCTACTAA	120
35	GGGAATCGAA TTTTCTTTCT CTTCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG	180
	CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACATG CTGGGTTTCC	240
40	CCATTCGGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG	300
	TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGCCCTTA ATAACCTAAT	360
	CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT	400

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(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 657 base pairs
50	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:

ACAACTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT 120  
 CAAATTTCTT ACGCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180  
 5 CTGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT 240  
 GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA 300  
 10 AGCCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360  
 CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420  
 CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT GAGGGAACtT TGAGCGCCTC 480  
 15 CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAACTGCCc GCcTGACACT GTCTACcmCC 540  
 ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600  
 CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60  
 TGGTATTACT GTTGCAAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120  
 35 GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCG 180  
 CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240  
 CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG 300  
 40 AAAAAGTGGG TAATGGTGCA GAACATAGTA AGACAATTAA TGTGTTTCGT GGTCAAAATA 360  
 ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACACACAT GGAAACGGCC 120  
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATAACACGT 180  
 5 AACACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240  
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300  
 10 AGTAACAAAA TAAGTTTGTG ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360  
 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60  
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTTCTAAGC GACCAATGTT 120  
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCACCTTATT TCATTAGTAT TCTTACCAGG 180  
 30 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240  
 TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300  
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTCCGT GTCGCAATTA 360  
 35 TGGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TGCGATGATT 420  
 GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480  
 CGATT 485

## (2) INFORMATION FOR SEQ ID NO: 3561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60  
 55 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240  
 AGGCATATGT TGTACCTATG ATGGTGGAAG AGCCTTCAGT TGTCGCTGCA GCTAGTTATG 300  
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAAACGGT ATCTTCTGAA CGTATTATGA 360  
 TAGGTCAAAT CGTCTTTGAT GGC GTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420  
 10 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463

(2) INFORMATION FOR SEQ ID NO: 3562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60  
 TTAATCTTGG TGCnGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120  
 25 TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG 180  
 TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240  
 CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTT CTTAATGCAT TGTCTAACAA 300  
 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360  
 AAAAAATATT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCg 420  
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480  
 TCCGATACGG CTACCTTGtT ACGACTTCAC CCCAATCATT TGTCACACCT TCGACGGCTA 540  
 GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600  
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180  
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240  
 5 TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300  
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTTT 360  
 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3564:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAGCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60  
 TAGTTGCCAT CATTAAGTTG GGCACCTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120  
 25 TGGGGATGAC GTCAAATCAT CATGCCCTT ATGATTGGG CTACACACGT GCTACAATGG 180  
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240  
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300  
 30 ATGCTACGGT GAATACGTTT CCGGGTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360  
 GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

35 (2) INFORMATION FOR SEQ ID NO: 3565:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTT GTAGCTATTT GTAACCTCTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60  
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTTGA 120  
 ATTCAATACA ATTGGTGTG ATGATGGAAT AGCTATGGGA CATATCGGAA TCGGATATTC 180  
 50 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAACG CTCATTGGTT 240  
 TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300



TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

## (2) INFORMATION FOR SEQ ID NO: 3566:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CatATTTAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60  
 CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120  
 CACCTATTGC ACGATTTCGT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGGTA 180  
 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGCTACTCAG CAATCTATCT GTTGAAGACA 240  
 TTGATTTGAT CGAATTGAAC GAAGCATTTG CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300  
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTCATCCAT 360  
 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTACtTAA TGAAATGGGT AGACGTCCCCG 420

## (2) INFORMATION FOR SEQ ID NO: 3567:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTGGTTTGG GACCAAGGGG TCGCAGGTTT 60  
 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120  
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TATTATTTAC 180  
 AAACATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTCATAC CCGTGAGGTC 240  
 GGGGGTTTGA TCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300  
 TAGCTCACTT GGTTAGAGCT AACGGCTCAT AACCGTTCGG TCGCAGGTTT GAGTCCTGCA 360  
 GGTCCCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

## (2) INFORMATION FOR SEQ ID NO: 3568:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

	TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT	60
10	TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTT GCGATTCCGT	120
	GTTTCAGAAA TCATCGGCAT CGCGTCATT C AATGATTCAT ATGCATCTAA AGCAATAGAA	180
	GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT	240
15	ACCGCAAAAA CAGTTGTCTC TGGAnTATAC ACACCTGATT GTTTTAATCC TTGTCTGACA	300
	TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATThA AAACCGCTTG ATGCGCCACC	360
20	ACAAGCCCCA CATTTCAGT GATGGCATGG nTGTGGGTTn	400

(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

	CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA	60
	GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG	120
35	CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG	180
	ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC	240
	GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC	300
40	TCTATCCAAT TGAGCTACGG GCGCATATGT TTTATTGAA AATGGTGCCG AGGACCGGAA	360
	TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTAAGTCC	400

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(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 542 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

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GTTTTTATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120  
 TTTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180  
 5 ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240  
 CGACCGCCCC AGTCAAACCTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300  
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaA GyTAGCGCTC 360  
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420  
 AGTAAAGCTC CACGGGGTCT TTCCGTCCTG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480  
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540  
 CG 542

## (2) INFORMATION FOR SEQ ID NO: 3571:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATA 60  
 aTaAAAATGT AAtGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCh GCGTGACAGG 120  
 CAGGCGTGTT AACCCTTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180  
 35 CACCGGACTT CGGGTTATGA GCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240  
 AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC CCGTTAAGGc CCTGTGCGTT 300  
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG GTAAATCGCT 360  
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420  
 CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480  
 45 CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540  
 TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTkCGA CCGAACGGTT 600  
 ATGAGCCGTT AGCTCTAAC 619

## (2) INFORMATION FOR SEQ ID NO: 3572:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60  
 5 GCAGAATTAA TTGATCAAGC GGTACTTCA TTGAGCCACA AGATTTATTC AGTGCGATGA 120  
 TTCGTGAAAT TGAAACGCAA GATTTGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG 180  
 10 TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240  
 TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300  
 AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360  
 15 TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3573:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

CAAATCGTAA CTCGCCGTT CATTCTACAA AAGGCACGCC ATCACCATT AACGGGCTCT 60  
 30 GACTACTTGT AAGCACACGG TTTCAGGTTC TATTTCACTC CCCTTCCGGG GTGCTTTTCA 120  
 CCTTTCCCTC ACGGTACTGG TTCACTATCG GTCCTAGAG AGTATTTAGC CTTAGGAGAT 180  
 GGCTCTCCCA GATTCCGACG GAATTTACAG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240  
 35 GAGACAACAT TTTCGACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC 300  
 GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTTA CAACCCCAAC AAGCAAGCTT 360  
 GTTGGTTTGG GGCTCTTCCC ATTTGCTCG CGGCTACTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3574:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1051 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60

5 TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180  
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240  
 10 GTCGAACTTA CGTTCCGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAT CCACAGTAGC 300  
 TCAGTGGTAG AGCTATCGGC TGTAAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360  
 GCCATGGCTC cTtGGTCAAG CGGTAAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420  
 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480  
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540  
 15 GAATAAGCTG GAGGGGTAGC GAAGTGGCTA AACGCGGCGG ACTGTAAATC CGCTcCTTCG 600  
 GGTTCCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660  
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720  
 20 GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780  
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840  
 ACCAAATGTG GTGGGtATAT AATTTAAAGA ACTATTTTTA AAATACAAC TTTAGAGCTT 900  
 25 TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960  
 CAAGCTGAAA ATCATCATTa TACGTGctTA AAGTGTGAAA TTTCTGTAAc CAAAAGAATn 1020  
 30 CACTTGATTA ATTnnATCTA TATAATGCCT C 1051

## (2) INFORMATION FOR SEQ ID NO: 3575:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

40 GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCGT 60  
 CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120  
 45 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT 180  
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240  
 50 AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300  
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360  
 AATAgGTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAnGTGAA 420

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## (2) INFORMATION FOR SEQ ID NO: 3576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

TTTGTTTCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG 60  
TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC 120  
GGGGCCCCAA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC 180  
CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAGGGCC 240  
CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC 300  
CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGGCCCAACA 360  
CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60  
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120  
ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC 180  
TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA 240  
GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTACAC TGCGGCTCTT CTGGGCGTTA 300  
ACCCTAAAGA GCACCCCTTC TCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA 360  
GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC 400

## (2) INFORMATION FOR SEQ ID NO: 3578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60  
 AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTGG GGTGAAGCCC TGTACCACCA 120  
 TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGAG TGCAATGGTA 180  
 10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTT 240  
 AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300  
 GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGTCTTC GCAATCCACG GATATACCTT 360  
 15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

## (2) INFORMATION FOR SEQ ID NO: 3579:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG ATCGAACCGC 60  
 30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120  
 AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180  
 CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC CCATAACCTC 240  
 35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGTACGGG CGCATATGTT TTTATTGAAA 300  
 ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360  
 TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 400

## 40 (2) INFORMATION FOR SEQ ID NO: 3580:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180  
 AACAAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240  
 5 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300  
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360  
 10 CCGTCTTCCA TGC GCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGGTACGGCT TTTCCAGAAG GATTACAAGG CCAAACATT GCACGAACGA 60  
 TTGCATTGCG TGC GGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120  
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180  
 CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA 240  
 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAGTCTG 300  
 30 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360  
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60  
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120  
 50 TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180  
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240  
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCCTTTTCTC 300



ATTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGT

400

(2) INFORMATION FOR SEQ ID NO: 3583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

15	AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC	60
	TAAGTGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT	120
	ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT	180
20	CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA	240
	CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG	300
	CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTGA CAACTCTCG TGGTGTGACG	360
25	GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC	400

(2) INFORMATION FOR SEQ ID NO: 3584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

	ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCACTGAT TCCTGGTTCA CTTGGTTTAT	60
40	CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG	120
	CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTTGG AATGATTCTA TCTTTAGCGA	180
	TGTGTTTACG TGAAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT	240
45	ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG	300
	ATATTTTCGA AATTCTATCT CAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC	360
50	AAACATTATT TGACAAAGTG TGGGACAGAC ATGTGTTATA	400

(2) INFORMATION FOR SEQ ID NO: 3585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC	60
10 TGTTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG	120
TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG	180
ACCGATACCT GGC GTTGACC CTCTTGCTT CGCAATCCAC GGATATACCT TAGTACCAGG	240
15 TAATTGACCA CCTTCACCAG GCTTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG	300
CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC	360
TTACTTTGGT GGCTTCCATC AACTTGTACT TCATAACGGT	400

20

(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC	60
TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG	120
35 AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA	180
CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT	240
ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCCG	300
40 CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT	360
TATGGGTCCT GTAATTGATG TTCGATTTGA ACATAACGAG	400

45

(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

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AGGATTGCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATGGTG CCGAGGACCG 240  
 GAATCGAACC GGTACGTGAT CACTCACC GC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300  
 CCGCCACCCC GGCACATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360  
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTTCG GACCTATTTT CTAATGCAGC 60  
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120  
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180  
 TAACTGGAAA GTCCTATTGA TGGATACTAG TAAACCATA TTTAGTAAAT ACAGATGGAA 240  
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAAG 300  
 ACGATATACT ACGACACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360  
 35 GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGACGGGT GAGTAACACG 60  
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120  
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGCACTTAT AGATGGATCC 180  
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360  
 GTCTTCGGAT CGTAAAACTC TGTTATTAGG GAAGAACATA 400

(2) INFORMATION FOR SEQ ID NO: 3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60  
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CGGGTGAGAA TCCCTCCACC GATTGACTAA 120  
 GGTTTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACAg 180  
 gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240  
 GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300  
 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360  
 TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420  
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480  
 AAGGAACTCG GCAAAATGAC CCCGTAACT 509

(2) INFORMATION FOR SEQ ID NO: 3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTGGGTAAAA 60  
 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120  
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GGCCTCTCC CAGCTGAGCT AAGCCCCCAA 180  
 ATAGGTATTA AATTAATGGT GGGCCTAAGT GGA CTGCAAC CACCGACCTC ACGCTTATCA 240  
 GCGCTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300  
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360

## (2) INFORMATION FOR SEQ ID NO: 3592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

5 TGGGnAACGC AACATCCTTT TCCAACTTAA CATATATTTT GGGACCTTAg CTGGTGGTCT 60  
 GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120  
 15 AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180  
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA 240  
 20 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300  
 ACGTAAgTCG GTTCGGTCCT CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360  
 ATCACCTGGT TTCCgSGTsT ACGACCAAAT AsTAAACGCC CTATTcAGAC TCGCTTTCCG 420  
 25 TAnGGCTCCA CATTACTGGn 440

## (2) INFORMATION FOR SEQ ID NO: 3593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTT TTTATTCCAT 60  
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAAC TTTGTTGAA GTGTTAGGAA 120  
 40 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180  
 GTACAGGTTT TGGTTTATGG TCATTTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240  
 TTATnTACTA CCCATTCCCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300  
 45 GTAAAGAAAG TAATTCAGAT TTAAAGAAA AAGTTGCAGC AAACCTTTGA TACGAAAAAA 360  
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

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## (2) INFORMATION FOR SEQ ID NO: 3594:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG	60
10 TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT	120
CCCCATTCCG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
15 TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT	300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAAATAA TTAACTCAT TGTCTGCTAA	360
ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAtTAATC CTCTCGCTC	409

20

(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

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AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT	60
GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTCAGCTGC TTCAAACAAT	120
35 ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TGCGCTTTTT CAATGCACTC	180
GTTGCAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAAC	240
TCATTTGCCT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC	300
40 CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG	360
GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA	400

(2) INFORMATION FOR SEQ ID NO: 3596:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 596 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

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CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCTCCA 120  
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180  
 5 TCTGCTTGTA AGGCAGATGC TCTCCAGCT GaGCTAATTC TCCAAAATAA TGACTCCTAC 240  
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300  
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360  
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 420  
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540  
 15 AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60  
 30 TACCCAGCTA TGCCGTGGC ACGACAACCTG GTACACCAGA GGTATGTCCA TCCCGTCTCT 120  
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180  
 GTCTCACGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240  
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300  
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG 360  
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180  
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240  
 5 ATTTCTGTGTT GCTAAAACAA CAGCATGTAT GCCATTGATA ACACCTTTAT TATGTGTTGC 300  
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATCGTTT GcaACCTCTT 360  
 CTCCAGTTCT CTCGCCCTT GGCTAAATCT TTAACAT 397

(2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCTTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60  
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC 120  
 25 GTTGAGCGAT GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180  
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC 240  
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300  
 30 TCAAAGTCC CGCCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360  
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60  
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120  
 50 GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180  
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240  
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300



GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA

400

## (2) INFORMATION FOR SEQ ID NO: 3601:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

15

ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60

GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120

AGTAAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180

20

ATTCATAAGA AATAATCGCT AGTGTTCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240

AATCTTTTAA TAAAAGAACG TAACCTCATG TTAACGTTTG ACTTATAAAA ATGGTGGAAG 300

25

CATAGGTTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG 360

GnCGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3602:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

GCTGTCTGAG TCGGAATCAC TGTnGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60

40

GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120

AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180

45

GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240

TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300

TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT 360

50

CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

## (2) INFORMATION FOR SEQ ID NO: 3603:

55

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

	TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTGCAATG AGATTGGAT CGTnTTTGTC	60
10	CACTACAATA TCTAATAGTT TTACTTTAAG TCCAGCATT CAAAAAGTG CTGCCAGTTG	120
	AGCGCCCAT GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC	180
	AATTTAGTTG AGGATAAGAT AACCATTAAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA	240
15	ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT	300
	TAAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG	360
	AAAGCmGaAT CTCCAGTCaA AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT	420
20	TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT	480
	AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CnTCTCAC	529

(2) INFORMATION FOR SEQ ID NO: 3604:

25

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

35	CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGG AAGCGATTGG TCGTCCTAAA	60
	ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA	120
	GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAT TGTAATACG	180
40	TTGTTTGACA ATGGCGCACT CGGACGTAA ACGAAACAAG GATTTTACAA AAAGGATAAA	240
	GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA	300
	CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA	360
45	TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG	399

(2) INFORMATION FOR SEQ ID NO: 3605:

50

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT 60  
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCTC 120  
 CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180  
 10 CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240  
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300  
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC TCCCCTTCCG 360  
 15 GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

## (2) INFORMATION FOR SEQ ID NO: 3606:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60  
 30 TAAAAACATA TGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGAAGAGGTT TCAAGAGGTT 120  
 ATGGGTTCGA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180  
 ACTTGTTTGG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240  
 35 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300  
 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAATAATA TAAGGCGGTG TAGCTCAGCT 360  
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3607:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

50 GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60  
 GTTTCCTTTC CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCCTTTTA 240  
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTCT TTCGAACACT AGCGATTATT 300  
5 TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC GGTTTTGCTT GGTAAAAATCT 360  
ATATTTTACT TACTTATCTA GTTTnCAATG TACAAATAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3608:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60  
TGCAAAaAGC CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA TTAATGGTGG 120  
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCT AACCAGCTGA 180  
25 GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240  
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300  
GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGC CCACCTTCGA 360  
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCCGGGTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3609:

- (i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAANTTCAAT CAGCAGAAGA ACTAGGACAT 60  
45 GGCGCTTTTA AAATTATTGA AACACATGCA TTAAAAGATG TACAAGCAGT ATTGGGTTTTT 120  
CATAATGACC CATCGGTTT GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180  
GCAGTAGATC GTTTTGAGTT TCATATTAAA GGCGTGGGTG GTCATGCTGC AAACCAGAAC 240  
50 AATGCAACGA TCCAGTTATT GTGTTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300  
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360

## (2) INFORMATION FOR SEQ ID NO: 3610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

```

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT      60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC      120
CCCATTGCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTGA      180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA      240
TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT      300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTAAAAATGA ATTTAACTCA TTGTCTGCTA      360
AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT      400

```

## (2) INFORMATION FOR SEQ ID NO: 3611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

```

GAGCTAGGCC GGCAATATGT AGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC      60
CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT      120
GGCAACGTTT TACTCTAGCG GAANTAGTT GNACTACCAT CGACGCTAAG GAGCTTAACT      180
TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG      240
TAATTTATAC ATTCAAAAC AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA      300
TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC      360
CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT      400

```

## (2) INFORMATION FOR SEQ ID NO: 3612:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60  
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180  
 10 GAACCACCGG ATCACTAAGT CCGTCTTTTC ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240  
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300  
 GnGCCTCCGT TACCTTTTAG GAGGCGACCG CCCCAGTCAA ACTGCCCCGCC TGACACTGTC 360  
 15 TCCCACCACG ATAAGTGThC GGGGGTTAGA AAGCCAACAC 400

## (2) INFORMATION FOR SEQ ID NO: 3613:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60  
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120  
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180  
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTCTT TTATAAAAAG ATTTAAACGC 240  
 35 GTTATTAATC TTGTGAGTGT TCTTTGGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300  
 TATTTAAAC TCTTTATTCA CTCGGTTTTC CTTGGTAAAA TCTATATTTT ACTTACTTAT 360  
 CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420  
 40 TTATCAGGCG TCGCTCTAA CCAGCTGAGC TATAGGcCCA TTTTTTTGaA TGTTAAATAA 480  
 ACATTCA 487

## (2) INFORMATION FOR SEQ ID NO: 3614:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG 60  
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120  
 5 CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180  
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240  
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300  
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360  
 CTCACGCGAG ATTTTAAGTC CTGTGCGTCT GcNAGTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3615:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120  
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180  
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240  
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300  
 35 TCTTTTCTCG TTTTCGTCAGA TTCAAACGTT TTCAC TTCG CAAGCCATTT TTCTTTGTGT 360  
 TTACTTTTTTA TTTTGACGTT TAGGCATAAA AAAAAGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 3616:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TnGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60  
 ATTCACTCGG TTTTGCTTGG kAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120  
 55 CAATTTCTTT TTAGTCAAGC GTCGCATAA GCAATATCAC TTTAACCAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGnGATCCAG CCGCACCTTC CGATACGGCT 300  
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360  
 5 TTACTIONCACC GGCTTCGGGT GTTACAAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

## (2) INFORMATION FOR SEQ ID NO: 3617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCCTTTATTC ACTCGGTTTT 60  
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAT TTCTTTTTTAG 120  
 TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180  
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT 240  
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTTACGACT 300  
 TCAACCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360  
 30 TCGGGTGTTA CAAACTCTCG TGGTGTGACG GCGGGTGTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60  
 45 ATACTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTGCGAGA 120  
 ATTTAGCTTT AACTATATCT TTTAGCCAA TCTTATTATG TATGTTGTGT TTGCGCTTGT 180  
 CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240  
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCAATAG TACTAATTTG TGCAATGTTT 300  
 GCAATTTGTT GGGTTGCATA TATCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360  
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA 60  
 CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC 120  
 TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180  
 ACCCGTCTTT CGCTACTCAC ACCGGCATTTC TCACTTCTAA GCGCTCCACA TGTCTTACG 240  
 ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300  
 CGGTAATATG TTTAGCCCCG GTACATTTTC GCGCGAGTGT CACTCGACTA GTGAGCTATT 360  
 ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

## (2) INFORMATION FOR SEQ ID NO: 3620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60  
 CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120  
 GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180  
 ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240  
 AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300  
 CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360  
 CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

## (2) INFORMATION FOR SEQ ID NO: 3621:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60  
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120  
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180  
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240  
 TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAACTGCC TGGCAACGTT CTA CTCTAGC 300  
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360  
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420  
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGT 475

## (2) INFORMATION FOR SEQ ID NO: 3622:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60  
 AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120  
 CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180  
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGGCGTT 240  
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACACATTT 300  
 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTGCAACAA TTGCTAGTTG GTGGATGAGT 360  
 40 TTTAAGTCAG TCGCTAAAGA TTGTGGAAG TAAGATCCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3623:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CaSACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTTCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180  
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240  
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300  
 TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360  
 10 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

## (2) INFORMATION FOR SEQ ID NO: 3624:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCTG AACCGCCGAC 60  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120  
 25 GGCAACGTTT TACTCTAGCG GAAnTAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180  
 TCTGTGTTCTG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240  
 30 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300  
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360  
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

## (2) INFORMATION FOR SEQ ID NO: 3625:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTGTGACC TCTAACAGCA 60  
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120  
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCCTCC TGATTGCTGT 180  
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTAACACC CATTCGTTTT 240  
 55 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

(2) INFORMATION FOR SEQ ID NO: 3626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

15 GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60  
 TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120  
 AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180  
 20 GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240  
 TTCCTTCCCG GAAGAGGTAT AGGTGCAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300  
 TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360  
 25 CCTATCTTCC GCTCCATAAT TTAATATTTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420  
 CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

(2) INFORMATION FOR SEQ ID NO: 3627:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

40 TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 60  
 AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT 120  
 45 TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 180  
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCGCAAG CCATTTTTCT TTGTGTTTGC 240  
 TTTTATTTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300  
 50 CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360  
 GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3628:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60  
 CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120  
 ATTTCTACG ACCCAGCAG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180  
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240  
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA 300  
 GCCTGTTATC CCCGGGGTAG CTTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360  
 20 CGGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA TCAATGGCAG GATTGAAAGG 60  
 35 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120  
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180  
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCAAGTAATT TCTTCTGGCT TTTCATCTTC 240  
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300  
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360  
 45 CTnTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TTTAAGTTGT nGATTTAAAA TATTAATAAA GTGTAAATTT GACTATTGAn ATTCKrACAA 60  
 ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120  
 5 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180  
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240  
 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTATG 300  
 10 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360  
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420  
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATrATATTT 480  
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540  
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

(2) INFORMATION FOR SEQ ID NO: 3631:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAAGTGAAC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60  
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGGC AATATGTAAG AATAAATGGT 120  
 35 GGAGAATGAC GGGTTGCAAC CGCCGACCCT CTGCTTGTA GGCAGATGCT CTCCCAGCTG 180  
 AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTCCG 240  
 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 300  
 40 CTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA 360  
 AAAGTGATTT GCTTCGCAA ACATTTATTT TGATTAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3632:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120  
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 180  
 5 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300  
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCAG CTGAGCTAAn GCCCCCAnAT AGGTATTAAA 360  
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

(2) INFORMATION FOR SEQ ID NO: 3633:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

25 ATATGTCAAC GTTAATTCCA AAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60  
 TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120  
 GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180  
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACCTCGG 240  
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300  
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360  
 35 CCAAGGCnAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

(2) INFORMATION FOR SEQ ID NO: 3634:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA 60  
 50 CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120  
 TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180  
 55 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTCGTCAGCT CCACATGTCA CCATGCTTCC 360  
 ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60  
 TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCAC TCGCCAAGCC 120  
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 180  
 GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240  
 CGTAAGTTGG GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT 300  
 CTTTCTCTT CTTGGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCTCTTT 360  
 TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTAGTCAA GCGCTCGCAT ACTGATTTTC 60  
 AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120  
 TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180  
 TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240  
 ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300  
 GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTCAACCCA nTCATTGTn CCACCTTCGA 360  
 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:



- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

10 AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGAATGTTA AATAAACATT 60  
 CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120  
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180  
 15 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240  
 CGGGTGTAC AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300  
 ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360  
 20 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 3638:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAGTAAGT CGAnCTACCA 60  
 35 TCGACGCTAA GGAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120  
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 180  
 40 TTTTGCTTCG CAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240  
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300  
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360  
 45 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3639:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 551 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAAGCAGC GATAAAAATA 60  
 ATCGCAATCG CTGGCAAACCT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120  
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCGA TAGCGTTGTA TAGCCAACGA 180  
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240  
 ACAAATCTCC ATAAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300  
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360  
 ATAaTGACCA TTTCCCAaT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420  
 15 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480  
 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAngTC GTAATTTTCCT 540  
 GATAGCCGGA T 551

(2) INFORMATION FOR SEQ ID NO: 3640:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

30 CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACCTGAT CCAACTTACA 60  
 CTACCAATAG AAACCTTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120  
 35 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180  
 TCCTATCATC CAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240  
 TCTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300  
 40 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360  
 TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGcAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120  
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180  
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240  
 CTAAGCTGAG GCCGACAGnG TAGGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300  
 AATCGTTTTA ATCGATGGGG GGrCGCATAG GATAGCGGAA CGTTGCCGATT GGATTGCACG 360  
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

## (2) INFORMATION FOR SEQ ID NO: 3642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTTA TAATCTTGTA 60  
 25 CAAATGCTTG CGCTACATCC TTGTGTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120  
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180  
 TTTCACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240  
 30 ATGCGGCTGG CATTTCTGCT GGCGACATTT CATGATAGCT AAAATGCCCC GGTtTAATCT 300  
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360  
 35 CAAAATGGkA ATCATCGCCA TTAtTATTAA ATTCaTTTAA GTGCATACCT TTTGTCCCA 420  
 TAATGACATT GCCTTCATG 439

## (2) INFORMATION FOR SEQ ID NO: 3643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCtTTATTCA CTCGGTTTTG CTTGGTAAAA 60  
 50 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120  
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAAA 180

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GCGTGCGCTC TAACCAGCTG AGCTATAGGC CCATTAAATT GAATGAACAA ACATTCAAAA 300  
 CTGAATACAA TATGTCACGT TATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360  
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnG GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTCCGATCG TAAAACTCTG 60  
 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120  
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180  
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240  
 25 AACCGTGGAG GGTCAATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300  
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360  
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

(2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATC 60  
 TTTCTTTGTG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120  
 45 CAATGCGGCT CATCGCATCC ACTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG 180  
 TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATnAT ACATTCAAAA CTAGATAGTA 300  
 50 AGTAAAGTG GATTTTGCTT CGCAAAACAT TTATTTTGA TTAAGTCTTC GATCGGATTA 360  
 GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAAA GAGTTTTAAA 60  
 TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120  
 GTTTAAATCT TTTTATAAAA GAACGTAAct TCATGTTAAC GTTTGACTTA TAAAAATGGT 180  
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CCGTGGATGC CTTGGCACTA GAAGCCrATG 240  
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300  
 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360  
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420  
 TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480  
 GGGTnTGTag GACACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540  
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600  
 TGaGTACGAC GGAGCACGTG AAATTCGGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660  
 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720  
 gGAAGGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

## (2) INFORMATION FOR SEQ ID NO: 3647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60  
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120  
 AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTTAAAG 180  
 AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240  
 ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

## (2) INFORMATION FOR SEQ ID NO: 3648:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

15 GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGAATTCCA TGTGTAGCGG 60  
 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120  
 TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180  
 20 GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCT TAGTGCTGCA GCTAACGCAT 240  
 TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC 300  
 CCGCACAAGC GgTGGaGCAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360  
 25 TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCCT TCGGGGGACA AAGTGACAAG 420  
 TGGTGCATGG TGTCGTCAAC TCCTGTCGTT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480  
 GCACCCCTTAA GCCTTAGTTT nCATCATTA GTTGGGCACT C 521

## (2) INFORMATION FOR SEQ ID NO: 3649:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60  
 TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120  
 45 ATACGTGTTT TAACACGTTT GTATCCCATT GCATCCATA ATTGGAATGG ACCAAGTTTC 180  
 CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240  
 ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300  
 50 TCGTCTTGcG CATTGAATAT GGTATCAAkG TTATGCACTA aGTCTTTATT AAATTCATT 360  
 AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGCGAA CCCCCGCGGn CCGTTAAGGC 60  
 CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120  
 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180  
 TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG 240  
 AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT 300  
 TCAGCCGGAC TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTGCGA 360  
 CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3651:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

TGGCGCTGTG CTTTAGTAA ACTATGGTCA TGTTGCGCTA AATGCAACCA TGCATGGTAA 60  
 AAACCTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120  
 GTCCATTTAA TCATTTGACG ATTCACCTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180  
 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240  
 GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTG AATGATTCAT ATATGATGGC 300  
 AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360  
 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

	CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC	60
5	GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC	120
	AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC	180
	TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC	240
10	TCCCAAGTTA AATTAATTGG CATTCCGGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC	300
	CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA	360
15	ATTTCGGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT	400

(2) INFORMATION FOR SEQ ID NO: 3653:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
20	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

	GGTTCGGTCC TCCATTCACT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG	60
	TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGCTCCA	120
30	CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG	180
	CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTAC	240
	TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG	300
35	AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT	360
	CGTACTCAAG nATCCACTCA AGAGAGACAA CATTTTCGAC	400

(2) INFORMATION FOR SEQ ID NO: 3654:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
45	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

50	AAAGGTCCTA AATATAATTT TACAATAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC	60
	CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT	120



GCGCTCTCCC AGCTGAGCTA AGCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240  
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCGTA 300  
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3655:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAA TCGATCAAAT CATCGATGAA GCGAAACATA 60  
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120  
 TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180  
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240  
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300  
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360  
 30 GACCATGACG AAATTGTAAG AGCGAGTGGA ATTAACCAA 400

## (2) INFORMATION FOR SEQ ID NO: 3656:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60  
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120  
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180  
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240  
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300  
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480  
GGGTCTGGGG CTTGGGTTCC GGTTCCTGGGT CTGGGACTTG GGTTCCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60  
GTTGATCTGT CCCGATTTGT TGGTAAACGG TTGATTAATG AAAATGTTTCG CGAAGGGATT 120  
CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180  
GAAACAAATT ATCATTTCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240  
CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300  
ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360  
GGATTCAATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 668 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60  
GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTGGCTTG GAGTAATAAA 120  
AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180  
GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240  
GAATTTGGTG GTAGTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300  
ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAAGAAA AACTTTCTCA ACAGCAAATT 360  
CmATTTCAAC AACGGAAAAA TCGCmACGTA TCTATATAAG GnGCGAACAG CTATGTGGTA 420  
ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

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TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600  
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCAGT 660  
 5 AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60  
 20 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120  
 TGGTGGCAGG CTATATTTCA GGTGCTTGA TTACGCAACT TATAACAGTA TTTAATGTCA 180  
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240  
 25 TTGGTGCGAC ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300  
 CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAAnGTG 360  
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCCAA CCTACTGATT 60  
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120  
 45 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180  
 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240  
 ACCATCGACG CTAAGGAGCT TAACCTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300  
 50 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA 360  
 GTGATTTTGT TTTGCAAAA CATTTATTTT GGATTAAGTC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

10	TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG	60
	GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTT ATTTTTCCTA CCGACAAGAA	120
	TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT	180
15	TTTTAACCAA AATTGATTA AAAAACTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG	240
	TTGCACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA	300
20	CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA	360
	AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA	400

(2) INFORMATION FOR SEQ ID NO: 3662:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

35	CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTCGAATG	60
	CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAA GCTTTTGTAT CAATTTTTTA	120
	TCGTCTTTTG TAATTTGCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT	180
40	TGTAATTCCT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG	240
	TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA	300
	ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA	360
45	CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAACTA	420
	ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG	480
	ATGACGTGTA CAAGCGCCGC ACGTTTTGCA GCGATTGAGC CGGCTAACT AGCTAAGATA	540
50	GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGATkGCTGC GTTTAAGCTA	600
	ATTAAATCTT GTTGATAAAA TTCTTGTAAT ATACCAATCG TCGCACTGA ACTTTGAACT	660

AGCATTAAAT TGGCTTnAAA TC

742

## (2) INFORMATION FOR SEQ ID NO: 3663:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT 60  
 TTTACTTACT TATCTAGTTT TCAATGTACA ATTTCTTTTT AGTCAAGCGC TCGCATACTG 120  
 CTTTATTTTC AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT AATTTTTCTT 180  
 AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG 240  
 CAATATCACT TTAACCAAAA AATATTTGAA TGTTAAATAA ACATTCAAAA CTGAATACAA 300  
 TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG 360  
 GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 3664:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 636 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTTTCTTT TTCATTATTA TCCATTATTT TTTCACCGCC 60  
 AAAACGAATT TCATGATGTT AATTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT 120  
 ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAKACATCAT TTAAAAGGAG 180  
 CTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AktGCTAGTA GTTGA CTGAA 240  
 TGAAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCAAC CACAGAGAAT 300  
 TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCAACA CAGAGAATTT 360  
 CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCACACA GAGAATTTTCG 420  
 AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT 480  
 CCCAaTTTCT ACAGACAATG CAAGTTGGCG GGGCCCAAC ACAGAAGCTG ACGAAAAGTC 540

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 404 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTCC	TGTTGCTAAA	ACAACAGCAT	GTATGCCATT	CATAACACCT	TTATTATGTG	60
TTGCTGCACG	ATGAATATCT	ACTTGGGCCA	ATACAGAAGC	ACGTTCCATT	CGTTTGGCAA	120
CCTCTTCTCC	AGTTCTCTCG	CCCCTTGCTA	AATCTTTAAC	ATCAATTTTCG	CCTTGAACCT	180
TAACAACGGA	CGCTGTTGCA	TGATTGGATA	AAATACTCAT	TAAAATGTCG	CTTTGGGAAA	240
tTCATTTTTT	AAAAATGCAG	TTATGGCCTC	TAAAATCGTA	TTAAGCATAT	TAGCGCCCCAT	300
AGCATCTTTC	GTATCAACAA	ATACTTTTAA	AGATAGTAAC	TGtTGcTCAG	GrAATGTakC	360
mAtCGCTATA	CGtTGgTAAC	CACCACCACG	CGCTTTAATA	GGAA		404

(2) INFORMATION FOR SEQ ID NO: 3666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCCAG	TAGCAATTAT	TGAACGATAT	TAGGCTATCT	AGTCGGCATA	TTTGTA AAAC	60
AAGATCCAAT	TAAATATCAA	CAGGAATAAC	GAATAATATA	AAAGAGGTTG	GGACATAAAT	120
CCCTAAAAAA	ACAGCAGTAA	GATAATTTTC	AATTAGAAAA	TATCTTACTG	CTGTTCTCTA	180
TTTATACAAT	ACTTCGTATT	GAATGGCTTC	GCTTTCCTAG	GGTGCCGTCT	CAGCCTCGGT	240
CTTCGACTGG	CAC TGCTCCC	TCAGGAGTCT	CGCCATTAAT	ACTACGTATT	AACGTGTAAT	300
TTTACTTTGA	AATACTTTAA	AAAAATAAGA	CAC TTTGCCC	AACTTGCACA	TAAATGTAAA	360
ATTCAATAAA	ATAAATTTCT	GTGTTGGATC	CCTnCGTATA			400

(2) INFORMATION FOR SEQ ID NO: 3667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

	CCAACAAATC TGTCTGTCGC ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC	60
10	CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA	120
	ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC	180
	CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG	240
15	GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA	300
	CCTTTTAAAG TATTACGTAA TGTGTGTGTG CGGTTTACAT CTTACCCAAA GTGCTAATGC	360
20	GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT	400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

	ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT	60
	AACATGACAT AACTCATGAC TGGGTTTCCC CATTCGGAAA TCTCTGGATC AAAGCTTACT	120
35	TACAGTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG	180
	CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT	240
40	TAATCTTGTG AGTGTCTTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT	300
	AAAACCTTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT	360
	TTTCAATGTA CAATTCTTTT TTAGTCAAGC GCTCGCATAA	400

45

(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120  
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGAAGT GGGCGGTTCG 180  
 5 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCTAA 240  
 GAGTGTAAG GCATAAGGGA GCTTGAAGTG GAGACCTACA AGTCGAGCAG GGTGAAAGA 300  
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360  
 CCGGGGGGAT AACAGGCTTA TCTCCCCCAA GATTTCACAT 400

## (2) INFORMATION FOR SEQ ID NO: 3670:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATCTTTC 60  
 25 TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120  
 GCGGCTCATC GCATCCACTT TTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTCTG 180  
 30 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 240  
 CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300  
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT CTTCCGATCG ATTAGTATTC 360  
 35 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCCGAACCT 400

## (2) INFORMATION FOR SEQ ID NO: 3671:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60  
 50 TTGAACGAGA TAAACAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120  
 AAATTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180  
 TAAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240



TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACChA nAGGnAGAAT 360  
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTTCG AGAAAGAACG 60  
 TAAATTTAAT cCTGATTTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120  
 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180  
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240  
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300  
 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360  
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAGGA GACTCGATTG TAGAAAAAGA 420  
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA 60  
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120  
 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCCAGC TGAGCTAAGC CCCCAAAnAG 180  
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240  
 TGGCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAAACTG 300  
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTTCCGAAT ATATCCTTAG 360  
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA 60  
 GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT 120  
 ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT 180  
 ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA 240  
 TCAGTAAGTA AACAGTGGTG GGTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA 300  
 TTGGAGGATG GAAATGATT ATGTACGCCA TTAACGTCAA ATTCCTTTGG CGTAAATGTC 360  
 TTTGTACCAA GTCAACAATC ATATACCAGT AGTCCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3675:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC 60  
 CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACCTGCCTG 120  
 GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT 180  
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240  
 TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300  
 TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT 360  
 CGGACCTATT AACCTCATCA ACCTTGAGGG ATCTTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 3676:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

EP 0 786 519 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

5 TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60  
 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120  
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180  
 10 GCCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCTGT ACCACCTATA ATCGTTTTAA 240  
 TCGATGGGGG GACGCATAGG ATAnGCGAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300  
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360  
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3677:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60  
 30 TATTTTCTT CTACTTTTGT TTTTCTGCG GCAATTTGTT GGTGAGTCGC ATCACCATTG 120  
 TTAATAACAT TTTGTGCATT TGTGATTCT GTTGACCCG CACGTTTAGC ATTTTCATAT 180  
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240  
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAT 300  
 TGCTTGCATT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360  
 TACTGTTCTT AATGGGCTTT TGAATAATA GCATTAGCGC 400

40 (2) INFORMATION FOR SEQ ID NO: 3678:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 648 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

ACAGTCAATT GnTCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60  
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

EP 0 786 519 A2

AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAAATATT GCGGGAGGCG GATTTGAACC 240  
 ACCGTACTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300  
 5 AAATAATGGC GGAGGAAGAG GGATTCTGAAC CCCC GCGGCC CGTTAAGGCC tGTCGGTTTT 360  
 CAAGACCGAT CCCTTCAGCC GGACTTGGGT ATTCTCCAT TATTATAGGT AAATCGCTAT 420  
 10 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480  
 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540  
 ACCCCCGCGA GCCGTTAAGC CCTGTGCGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600  
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

(2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60  
 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120  
 30 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTCCGAT GACAGCTTCT 180  
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240  
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTGTGTC AATTCAAACG TGTACTTTCC 300  
 ACCGTTTTTC ATTTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360  
 TTCAATAAGT TGTTTTCTCA ATTTAAAATC AAGTTCTTTC 400

(2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAANTAAAG 60  
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120

TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTTATT 240  
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300  
 5 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360  
 CGCTTGGCTT CTnTCCTCTC CTTCGGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

20 TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 60  
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTCGCCAAG CCATTTTTCT TTGTGTTTAC 120  
 TTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180  
 25 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240  
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCAIT TAGCTCTACT 300  
 30 AAACGTTG CGCTCTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360  
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 414 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

45 TTGAACATGT TGAATCTAAT GAAATTCCTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60  
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120  
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTGAGTAT AACGAGATTT 180  
 50 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240  
 TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300  
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

## (2) INFORMATION FOR SEQ ID NO: 3683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

TTGGAATTC TCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTTCGGT 60  
 CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT 120  
 CTACGACCAA ATACTAAACG CCCTATTCAG ACTCGCTTTC GCTACGGCTC CACATTTACT 180  
 GCTTAACCTT GCATCAAATC GTAACGCGC GGTTCATTCT ACAAAGGCA CGCCATCACC 240  
 CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCTTC 300  
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGGTTTAC TATCGGTCAC TANGAGAGTA 360  
 TTAAAGCCTT ANGAGATGGT CCTCCCAGAT TCCCGACGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

GATnTATGAT GAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT 60  
 TCACTTATAC TTCTAGTCAC AGATTnAAAT AATCAAAAGT GCACATTATT AAAATATCAA 120  
 TTTCACACTC AATGCGGCTC ATCGCATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG 180  
 GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTCTT GACTTgTGAC AATCGCTTGC 240  
 TTCTTTCTCT TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC GTTGCCTCTT 300  
 TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT TTTGTGTTTA 360  
 CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTGCCTGGG 420  
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA 480  
 CTTGTGACAA TCGCTTGCTT CTnTCCTCTC CTTCGGCTCT CGGTACT 528

## (2) INFORMATION FOR SEQ ID NO: 3685:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

10 AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60  
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120  
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180  
 15 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240  
 TTCAGTGC GA TGATTCGTGA AATTGAAACG CAAGATTTTCG ATATAGAGCA TCTAGCGACG 300  
 GCGATTGCGA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360  
 20 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3686:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 403 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCCT CTTCGGTGGT 60  
 35 GCAGTTGCGA CAACTATGGG TTGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120  
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180  
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240  
 40 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300  
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360  
 GATTTTAAAT TATTgAAAAT AAACCATATA CAGGTGCAAC GGT 403

45

## (2) INFORMATION FOR SEQ ID NO: 3687:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 449 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCCGCGAT AATAAAAAAT AATGGCGGAG 60  
 GAAGAGGGAT TCGAACCCCC GCGGCCCGTT AAGGnCTGT CGGTTTTCAA GACCGATCCC 120  
 5 TTCAGCCGGA CTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180  
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240  
 ACCGCTACAC TACGAGACCA TTAGTAAAC GGAGGAAGAG GGATTGGAAC CCCGCGAGC 300  
 10 CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360  
 AAATTATATG GACCTTGCA GACTCGAACC TCGACCGAA CGGTATGAGC CGTAGCnCTA 420  
 ACCACTGGGC TAAAGTCCTA ATATAATT 449  
 15

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAA TTGAAGGTGC CAAGGTGTT ATTCAAGGTT TcNATAATGC 60  
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120  
 30 TGCTTACGGT GCATTACAG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180  
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240  
 TGAATTAGAT TGTGACATT TAGTACCAGC GGCTATTTCA AACCAAATTA CAGAAGACAA 300  
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360  
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAAT TTGAATGAAC 60  
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATTCGCG ATCTTCTGAA GAAGATGTTT 120



CGACTTCACC CCAATCATTT GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240  
 CGGCTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300  
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360  
 TGCAGACTAC AATCCGAACT GAGAACnACT TTATGGGGAA 400

## (2) INFORMATION FOR SEQ ID NO: 3690:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 553 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

20 GCnGCGTTTT AGGCCCATTC GGTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60  
 TGAACCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120  
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180  
 25 CAACTGAGCT ACTGAACCAT AATAAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240  
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300  
 TTGCGGGAGG CGGATTTGAA CCACCGactt CGGGTTATGA GCCCGACGAG CTACCGAACT 360  
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC 420  
 CCGTTAAGGC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480  
 ATTATTATAG GTAnATCGCT ATTAATTATA AnATTAAAT GCGGTCTCG ACGGGAATCG 540  
 35 AACCCGCGGA TCT 553

## (2) INFORMATION FOR SEQ ID NO: 3691:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60  
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTTG TG ACAATCGCTT GCTTCTTTCC 120  
 TCTTCTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300  
 ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360  
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 410 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG ATTGAGTATA 60  
 20 TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120  
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAAACA TATCGCGAAA 180  
 TATCATTTTG AGAATTCTAA CGAATTTCCT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240  
 25 ATTTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300  
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGgAAA 360  
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

30 (2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60  
 TTTTATTTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACAACATGC 120  
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTTCTTAG ATTGTGCTTT 180  
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCa ATAACAGGTG TTACTACTTT 240  
 ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300  
 50 ACCAGGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTTGGT GTTTCCGGCT CGCTTGGTAC 360  
 TTCTGGTGTC GGTGGTGTG GGTGTTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCCGT 420

## (2) INFORMATION FOR SEQ ID NO: 3694:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60  
 ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120  
 ATTAGCTACG GTTTCCCGAA GTTATCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180  
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCAATG 240  
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300  
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360  
 AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCTGTGTC 60  
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTGAAGCG GAATCAGGGA GTGGTTCAGT 120  
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAAT GGTCTTTTAA 180  
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240  
 CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC 300  
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360  
 TTGGTATAAC TTAATTTChC CTTTTCCTTC ATChGGTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3696:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60  
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120  
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180  
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240  
 CATTTTTATA AGTCAAACGC TCACATACGG CTTTCGTTTC ATTATTTTAA ATGCTCATT 300  
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360  
 15 TAAAAAGATT TAAACGCGTT GATTAACTG TGAGTGTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3697:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60  
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120  
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180  
 TTGACGGCT AGCTCCTAAA AGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240  
 35 TGTGACGGGC GGTGTGTACA AGACCCGGA ACGTATTAC CGTAGCATGC TGATCTACGA 300  
 TTACTAnCGA TTCCAnCTTC ATGTAGTCGA GTTGACAGACT ACAATCCGAA CTGAGAACAA 360  
 CTTTATGGGA TTTGCTTGAC CTCGCGGTTT CGCTnCCCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3698:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

50 AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

CCCCATTTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAGCA TATCGTCGTT 180  
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240  
 5 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC 300  
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAACTC TTTATTTACT CGGTTGTGCT 360  
 TGGNAAAATC TATATTTTAC TTACTTATCT AGGTTTCAAT 400

(2) INFORMATION FOR SEQ ID NO: 3699:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCAG TTGCAAATCC 60  
 AAATTCTTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACCTACC 120  
 25 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180  
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC 240  
 TGTAAACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA 300  
 30 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360  
 CGCATTTTTT AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3700:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCGTGTGT TCGGCATGGG AACAGGTGTG 60  
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120  
 TAAGTAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180  
 50 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAAACC TCATCATCTT 240  
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnC GGGGGGCTTC ATGCTTAGAT 300

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

## (2) INFORMATION FOR SEQ ID NO: 3701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

AACCAAGCCC AATAATGGAC TGGCCGCCTA ATAATAAAG CTCTAAAAGT TGTATTTTAA 60  
 AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT 120  
 CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180  
 TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC 240  
 GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300  
 TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGnTT TACAGTCCGC 360  
 CGCGTTTAGC CAnTTCGnTA CCCCTCCAGn TTATTCATAT 400

## (2) INFORMATION FOR SEQ ID NO: 3702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60  
 CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAACTACTT 120  
 CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180  
 TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240  
 ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300  
 CGGCCAGAGG ACTTGGAACC CCCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360  
 GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

## (2) INFORMATION FOR SEQ ID NO: 3703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

	CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT	60
10	ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAACT	120
	AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGc GCTCTCCAG CTGAGCTAAG	180
	CCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCTG AACCTGCGAC CCCTTGGTCC	240
15	CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG	300
	TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG	360
	CATATGTTTT TAATTGAAAT GGTGCCCCGAG GACCGGAATG	400

20

(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

30

	CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAATTATT ACGTCAGCTT	60
	ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG	120
35	TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTCAG	180
	CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA	240
	GCACTCGCGG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT	300
40	AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAA GGTAACTA	360
	TCATTTATGC AATACGGCGC ATTACCCAGA GTTGCATGGT	400

(2) INFORMATION FOR SEQ ID NO: 3705:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 478 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

55

TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120  
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCITTTCCCCT TCGGGGGTAC 180  
 5 AAAGTGACAG GTGGTGCATG GTTGTCGTCA GCTCGTGTG TGAGATGTTG GGTAAAGTCC 240  
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300  
 10 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAAA TCATCATGCC CCTTATGATT 360  
 TGGGgCTACA CACGTGTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420  
 AATCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

(2) INFORMATION FOR SEQ ID NO: 3706:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

25 ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60  
 TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTGCGA 120  
 30 TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180  
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240  
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCCAAAAGG TCATGCTGAA ACGTTGAAAn 300  
 35 CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360  
 AAGCAGTAGA AGATGTTCCA TAACTTTGG TGAGGACCCT 400

(2) INFORMATION FOR SEQ ID NO: 3707:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

50 GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60  
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAAATCGAA CCCGCGATCT CCTGCGTGAC 120  
 AGGCAGGCGT GTTAACCGCT AACTACGAG ACCTATAAAA TATTGCGGGA GCGGATTTG 180



TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCCGC GGCCCCGTAA GGCCCTGTCTG 300  
 GTTTTCAAGA CCGATCCCTT CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC 360  
 5 GCTATTAATT ATAAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCCAT TAAAGCGGTA CCAnGCTGGG TTCAGAACGT CGTGAGCAnG TTCGGTCCCT 60  
 20 ATCnGGGGTG GCGGTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120  
 GACATACCTC TGGTGTACCA GTTGTCGTGC CAACGGCATA GCTGGGTAGC TATGTGTGGA 180  
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCTC AAGATGAGAT TTCCCAACTT 240  
 25 CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300  
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360  
 30 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAAT ACTATTAAGA AGTCCTGAAA 60  
 AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120  
 45 CAGTGTGTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTGTGTTCT 180  
 TGCAACGCTA TTTAGTATCA GGTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATTy 240  
 50 GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300  
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360  
 CCAAGTTTAC AAAAAGTTGA AAATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTTCGAA 420

## (2) INFORMATION FOR SEQ ID NO: 3710:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

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AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC      60
CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT      120
TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT      180
TTTAAGTCTT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA      240
CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC      300
TGCAATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG      360
TGCCTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG      420
ACCCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG      480
GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT      540
AACCAATTTG AGCTAAGGC                                         559

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## (2) INFORMATION FOR SEQ ID NO: 3711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

```

AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG      60
GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC      120
TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTTATT      180
CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACC CCTGATAAGC GTGAGGTCCG      240
TGGTTCGAGT CCACTTAGGC CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC      300
TGGGAGAGCG CTGCTTTTGC ACGCAGGAGG TCAGCGGTTC GATCCCGCTA GTCTCCACCA      360
TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAATAT                                         400

```

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

TAGAATGAAC	CGGCGAGTTA	CGATTGATG	CAAGGTAAAG	CAGTAAATGT	GGAGCCGTAG	60
CGAnnTCATG	TCTGAATAGG	GCGTTTAGTA	TTTGGTCGTA	GCCTGAAACC	nnGTGATCTA	120
CCCTTGGTCA	GGTTGAAGTT	CAGGTAACAC	TGAATGGAGG	ACCGAACCGA	CTTACGTTGA	180
AAAGTGAGCG	GATGAACTGA	GGGTAGCGGA	GAAATTCCAA	TCGAACCTGG	AAATAGCTGG	240
TTCTCTCCGA	AATAGCTTTA	GGGCTAGCCT	CAAGTGATGG	ATTATTGGAG	GTAGAGCACT	300
GTTTGGACGA	GGGGCCCCCTC	TCGGGTTACC	GAATTCAGAC	AAACTCCGAA	TGCCAATTTA	360
ATTTAACTTG	GGGAGTCAGA	ACATTGGGTG	ATAAGGTCCG			400

(2) INFORMATION FOR SEQ ID NO: 3713:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

TTTTTAAGTC	TGATGTGAAA	GCCCACGGCT	CAACCGTGAA	GGGTCATTGG	AAACTGGAAA	60
ACTTGAGTGC	AGAAGAGGAA	AGTGGAATTC	CATGTGTAGC	GGTGAAATGC	GCAGAGATAT	120
GGAGGAACAC	CAGTGCGCAA	GGCGACTTTC	TGGTCTGTAA	CTGACGCTGA	TGTGCGAAAC	180
GTGGGGATCA	nACAGGATTA	GATACCCGGT	AGTCCACGCC	GTAAACGATG	AGTGCTAAAG	240
TGTTAGGGGG	TTTCCGCCCC	TTAGTGCTGC	AGTAAACGCA	TtnAAGCACT	CCGnCTGGGG	300
AGTACGnCCG	CAAGTTGGAA	ACTTCAAAGG	AATTGACGGG	GGACCCGCAC	AAGCGTTGGG	360
AGCATGTGGT	TTAATTTCGA	AGCAACGGAG	AGGAACCTGA			400

(2) INFORMATION FOR SEQ ID NO: 3714:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAAnt CGACTACCAT 120  
 CGACGCTAAG GAGCTTAACT TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180  
 10 AGTCACCAGA CATATGAATG TAATTTATAC ATTCAAACCT AGATAGTAAG TAAAAGTGAT 240  
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300  
 catGTCACCA TGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360  
 15 CCGAAGTTGG GAAATCTCAT CTTGAGGGGG GCTTCATGTC TTAGCATTTC AGTCACTTAT 420  
 GCCCCG 425

## (2) INFORMATION FOR SEQ ID NO: 3715:

20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTGTAGG TTTGTCATGC 60  
 CCAGTTACAA GTTGCGTTAT CGTAGACACT AACATTAATA TGAAGGTAA TGTTGCTGTT 120  
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTGG TGCACCTAAC 180  
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTTTGTGC ACTTTGTTAA 240  
 ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATAA GTAATACATC 300  
 TCCAACATTT GCCTTTAATT CTTTTCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360  
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT AnGTAGTCCT 400

## (2) INFORMATION FOR SEQ ID NO: 3716:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT 60

5 GCAATATCAC TTAAACCAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180  
 ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240  
 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTG 300  
 TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTIONACC GGTTCGGGT GTTACAACT 360  
 10 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60  
 25 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120  
 GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180  
 TACCGTGAGG AAAGGTGAAA AGCACCCTCG AAGAGTTGA AATAGAACCCT GAAACCGTGT 240  
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300  
 CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA GCCGTAGCAN AANNGTGTTCT 360  
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

35 (2) INFORMATION FOR SEQ ID NO: 3718:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60  
 AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120  
 50 AGGCTCATAC AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180  
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240  
 GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAATAAGT 300

55

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGThA

400

(2) INFORMATION FOR SEQ ID NO: 3719:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

15	ATTTAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA AGThGAGCTA CCATCGACGC	60
	TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC	120
	CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT	180
20	TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT	240
	CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA	300
25	GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT	360
	CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAnGG	400

(2) INFORMATION FOR SEQ ID NO: 3720:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

40	CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT	60
	TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC	120
	TTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA	180
45	AACATGATAA TGCAATGGCG GAACTTCACC GATGTCAATT AAATATACAG CTACAACATG	240
	TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT	300
	CACAATTTCA TTTTGCGTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA	360
50	CTATAACCTC GGGAAATATT GTGTTTGAAA TGGGCACGCC	400

(2) INFORMATION FOR SEQ ID NO: 3721:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

	AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG	60
10	GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT	120
	GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC	180
	AGCCGAAAAT GGATGGTGTT AAGAGCGTTA CTTGGTTTGG CCGTATGCTT ATTTTAAATG	240
15	GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG	300
	TGGTGTGTGT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GCGGCCACTG AnAGATCGTG	360
20	GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCAGCGCA	400

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

	TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA	60
	TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT	120
35	GGATTGGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT	180
	TAATAATAAG GCGCGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT	240
	GTTAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG	300
40	GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCTTA TTAAATGAT AAATGGAGGG	360
	GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC	400

45

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

55

GGTTCAAGTC CTCTGGCCGG CACCATTtTtT GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120  
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180  
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTCG 240  
 ATTCCTACTG CCCCTGCCAT GCGGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300  
 10 CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360  
 GGTAAGGCAA CGGACTTTGA CTCCGTCCT CGTTGGTTCG 400

## (2) INFORMATION FOR SEQ ID NO: 3724:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60  
 25 ATATGGCGTG CGTCGTTTTG ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120  
 AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TtTGTCATTC 180  
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240  
 TGGGTGCGGG TATTAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300  
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360  
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

## (2) INFORMATION FOR SEQ ID NO: 3725:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60  
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120  
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180  
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240



CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360  
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420  
 5 CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGGC TCATCTGATG TTTCTT 476

## (2) INFORMATION FOR SEQ ID NO: 3726:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60  
 20 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120  
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTITAGAC 180  
 CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240  
 25 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTTCAG GTTCAACTTG 300  
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360  
 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

## (2) INFORMATION FOR SEQ ID NO: 3727:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60  
 ATGGGCGAAC AGCAAACCCT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120  
 45 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180  
 GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240  
 50 GTCTTTTCGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCCTTATG CCTTTTACAT 300  
 CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTTAGGAG 360  
 GCGAACGGCC CCAGTTCAAA CTGCCCCCCT GAACACTGTC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG 60  
 GTGTGTCAIT TGAGTGTCCA ATCGGTGCGA CGATTGCGAT TATCGGAGAA AGTGGTAGCG 120  
 GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTGTGTGTA 180  
 CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT 240  
 TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG 300  
 TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT 360  
 TGAAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3729:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCAGC GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC 60  
 TTATATAGTT TGTAATAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 120  
 TGCAAAAGC CGCTCTCCCA GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA 180  
 GACAGGTTTC AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC 240  
 TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA 300  
 AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC 360  
 CGGAATCGAA CCGTAGTGA ATCACTCACC GCAGATTTTA 400

(2) INFORMATION FOR SEQ ID NO: 3730:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

5 ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60  
 CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CTATGTTTCC 120  
 ACCATTTTAA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC 180  
 10 GCGTTATTAA TCTTGTGAGT GTTCTTTCGA AACTAGCGA TTATTTCTTA TGAATTC AAG 240  
 CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTAATTACTT 300  
 ATCTAGTTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360  
 15 GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

## (2) INFORMATION FOR SEQ ID NO: 3731:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi). SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 60  
 30 TGGAGAATGA CGGGTTCGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCAGCT 120  
 GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180  
 GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT 240  
 35 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT 300  
 AAAAGTGATT TTGCTTCGCA AACATTTTAT TTTGATTAA GTCTTCGATC GATTAGTATT 360  
 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

## (2) INFORMATION FOR SEQ ID NO: 3732:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

50 CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60  
 TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

EP 0 786 519 A2

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240  
 ATATTTATTA ACTGGTGACT TAGCGAgATG GACAACGATG GCGATATATT TATTATTGAC 300  
 5 CGCAAAaAAG AaTTAATCAT AACTGGTGgc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360  
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

(2) INFORMATION FOR SEQ ID NO: 3733:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60  
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120  
 AAGACGGCAA AGTGGGTTCT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180  
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240  
 ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300  
 TACCAGGTAT TTTTGACGCA GGnGATGTTT GCGACAAAGG TTACGCCAAA TTGTCACTGC 360  
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3734:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60  
 45 CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120  
 TTGATAAACA GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180  
 CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 240  
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT 300  
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGAct CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCCT CCAAAATTAT ATGGACCTTG CAGACTCGAA 60  
 CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120  
 TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA 180  
 TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240  
 TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCAGCT 300  
 GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGGAAGA CAGGATTCGA ACCTGCGACC 360  
 CCTTGGTCCC CAAACCAAGT GGTnTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAAATAA TGGCGGAGGA 60  
 AGAGGGATTG GAACCCCCGC GGCCCGTTAA GGCCCTGTGC GTTTTCAAGA CCGATCCCTT 120  
 CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAAAT ATAAAATTAA 180  
 ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240  
 CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 300  
 TTAAGCCCCCT GTCGGTTTTT AAGACCGATT CTTTCAGCCG GACTTGGGTA nTnTCCAAA 360  
 ATTATATGGA CCTTGCAGGA CTCGAACTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC	60
10	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC	120
	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
15	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG	300
	ACGGGATTTCG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACTACTT	360
20	CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA	400

(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

	AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAAG CAGATGCTCT CCCAGCTGAG	60
	CTAATTCTCC GATTTAAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGAnCT	120
35	ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT	180
	GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AAAC TAGATA GTAAGTAAAA	240
	GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG	300
40	CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT	360
	TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT	400

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(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

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CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA CCGACATCTT 120  
 TAATTAATTG CTnTGACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180  
 5 TCATGTTATC TTCAATCGTT TCACCAACA AGTCACTTTG CTGCATCAA TAACTGATTC 240  
 GTTGACGCAA TTCTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300  
 CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360  
 10 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3740:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60  
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTCA CTTGCCAAG CCATTTTCT 120  
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 TGCGGCTCAT CGCATCCaTT TTTGCCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240  
 30 TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AACTCGTTG CGCTCTTTTC TCGTTTCGTC 360  
 35 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTtCTTG TGTtTGCTT TnA 413

## (2) INFORMATION FOR SEQ ID NO: 3741:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60  
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGTCTCTCT CGTACTAAGG ACAGCTCCTC 120  
 50 TCAAATTTCC TACGCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180  
 GCTCGCGTAC CGCTTTAATG GCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360  
 ACCGGATCAn TAAGTCCGTC TnTCGACCCT GntGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60  
 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120  
 CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180  
 CATCTGCCTT ACAAGCAGAG GGTGGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 240  
 TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300  
 GGTTCAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360  
 GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60  
 TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120  
 TGTATGTAGT ATTGTTACGT TCTTGTCGGA AATAACGATA CACTTGCGTT TCTTTACCAA 180  
 CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240  
 TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300  
 CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360  
 ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:



- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10 CTACTGATTA CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60  
 ATGGTGGAGA ATGACGGGTT CGAACCGCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120  
 AGCTGAGCTA ATTCTCCGAT TTAAACTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 180  
 15 GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240  
 ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT 300  
 AAGTAAAAGT GATTTGCTTC GCAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360  
 20 TCAGCTCCAC ATGTCACCAT GCTTCCanCT CGnACCTATT 400

## (2) INFORMATION FOR SEQ ID NO: 3745:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60  
 35 AAAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT 120  
 CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACGCG GTTTTGCTTG GTAAATCTA 180  
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240  
 40 CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300  
 TTAATGCATT GTCTAACAAAC CGCTTGCTTT AAAAGAATA GATTGnCAAG CGCTCGCATA 360  
 AGCAATATCA CTTnAACCAA AAAATA 386

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## (2) INFORMATION FOR SEQ ID NO: 3746:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 677 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60  
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120  
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTCTGACCG AnaACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240  
 10 TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300  
 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360  
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420  
 15 tTACCAATTc AGACAAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480  
 TGATAAGGTC CGTGTTCGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540  
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600  
 20 CCATCATTTT AAAGAGTGCG TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660  
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCAGC GTATTGCCTT TGAATCGCAT GCACAAAATA 60  
 TGATGCTCAT TCATGAAAAT GGTGCGCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120  
 GTGTTCGTTT TAAGCGTGAc ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180  
 40 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240  
 AGTACGCGAC TTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300  
 45 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360  
 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

5 ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60  
 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120  
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180  
 10 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG 240  
 ATCGATTAGT ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300  
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360  
 15 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3749:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

25 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120  
 30 GTTTTAGGCA TAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180  
 TGCCTGGCAA CGTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240  
 35 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATT 300  
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360  
 GCCAAGCCAT TTTTCTTTG TGTnTACTTT TTAATTTTGA 400

## (2) INFORMATION FOR SEQ ID NO: 3750:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

50 ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC 60  
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240  
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC 300  
 5 GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360  
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

20 CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCCTATAA 60  
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120  
 CCGCTGAAC TCTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTnA 180  
 25 GnATTCTTAA GTCTAGTGCG TCTGCCAATT CGCCACACC CGCAAATGGT GAGCCATAGA 240  
 GGATTGGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300  
 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGAACCCCC AACCTACTGA TTACAAGTCA 360  
 30 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

45 TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60  
 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120  
 CTAAGTGCCT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180  
 50 GGCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240  
 AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATa 300  
 AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360  
 55

## (2) INFORMATION FOR SEQ ID NO: 3753:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA	60
GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT	120
TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC	180
TCTTTTCTCG TTTTCGTCAGA TTCAAACGTT TTTCACTTCGC CAAGCCATTT TTCTTTGTGT	240
TTACTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGC GGTC TCAATGCGGC	300
TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA	360
TCGACGCTAA GAACCTTTCT TGACTGGTGA CAAnCGCTTG	400

## (2) INFORMATION FOR SEQ ID NO: 3754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGA CTCGnACCAC	60
CGACCTCAGC CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTAATTTGA	120
ATGAnCAAAC ATTCAAAAC GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG	180
ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC	240
TTGTTACGAC TTCACCCCAA TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA	300
CTCCACCGGC TTCGGGTGTT ACAAACCTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC	360
GGGAACGTAT TCACCGTAGC A	381

## (2) INFORMATION FOR SEQ ID NO: 3755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60  
 CCCC GTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120  
 CATGAAGTTA CGTTCTTTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTTCT 180  
 10 TTCGAACATA GCGGATTATT TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCT 240  
 GGTTTTGCTT GGTAAAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300  
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360  
 15 AATATTTGGA ATGTTnAAAT AAACATnCAA AACTGAATAC 400

## (2) INFORMATION FOR SEQ ID NO: 3756:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60  
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120  
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180  
 35 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240  
 ACTTAACATA TATTTTGGA CCTTAGCTGG TGGTCTGGG CTTTCCGGn GGGGnACACG 300  
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG ATTTGTCTGA 360  
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3757:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 458 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC 60

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EP 0 786 519 A2

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180  
TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT 240  
5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300  
AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAArTttGG GAAtCTCATC TTGAGGGGGG 360  
gCTCATGctT AGATGCTTca GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420  
10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

(2) INFORMATION FOR SEQ ID NO: 3758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60  
25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTAAAAAGA ATAGATTGTC 120  
AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA AATAAACATT 180  
30 CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240  
ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300  
ACCCCAATCA TTTGTCCAC CTTGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360  
35 GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

(2) INFORMATION FOR SEQ ID NO: 3759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG 60  
50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAGGTCC TAAATATAAT TTTACAATA 120  
ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180  
TAGCCAGCTG AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360  
 AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60  
 ACCAGAGGTA TGTCCATCCC GGTCCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120  
 CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTT TGAACCCAGC TCGCGTACCG 180  
 CTTTAATGGG CGAACAGCAA nCCCTTGGGA CCGACTACAG CCCCAGGATG CGATGAGCCG 240  
 ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA GCCTGTTATC 300  
 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GnCCTTnCAT GCGGAACACC GGATCACTAA 360  
 GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

TATGTATTTT ATAATGTACA GTCGTTGAn TCnTATTTT CTTATATTA AGTGCCATTA 60  
 ATACAAAACC TAGCTCTCGT TTAACTTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120  
 CAAAATAGCC TTCATAAATC CAAAACAGG CTCTACATCA ATTTTCTTT GACTATAGAT 180  
 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240  
 ATAATTCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300  
 AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360  
 ATCATTACGG TATGCATATC TTTTAAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420  
 ATCATTAAAGT TCGTCATATT TCCAATTTTA AGTGTTGAAA ATGTCACTTT TAACTTTCT 480



AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600  
 AATAACCGAG GGATTGTTGG AAT 623

(2) INFORMATION FOR SEQ ID NO: 3762:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAA TAGTTCTTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60  
 AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCTGA ACCTCTGACC 120  
 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180  
 CTGGATTCTGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240  
 CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300  
 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360  
 CaAAATGGTG GaGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420  
 TCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480  
 CCGTGAAAGG GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540  
 CGAACCTTAC GACCGATCGG TTAAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600  
 ATTAATATTA TGCCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660  
 ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60  
 AAAAATGGAG CAGAAGACGG GATTCTGAACC CGCGACCCCA ACCTTGGCAA GGTGTATTTC 120  
 TACCGCTGAA CTACTTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

EP 0 786 519 A2

AGGATTGCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300  
GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCA ACCTACTGGA TTTACAAGTT 360  
5 CAATTGCTCT AnCAATTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCGA ATTTGGTTTC 60  
20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120  
CGTTTAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAACCTAT TCTTTTGTTA 180  
TTAGGACATA TAAATTCATT ATTAAGTTG TCATATTTCC AATTTTGAGT GTTGAAATG 240  
25 CCACTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300  
TTATTAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360  
ACAATATACT CTGGTAAATA ACCGAaGGaT TTTGAATCAT TGTTAAAAAT GGGATTAATG 420  
30 TTCTAGTATC TGTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTGr GAATTTGTCTG 480  
CTATTTGgTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTCCATATG GGCCTTCCTT 540  
35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTAGGAAA ACCTAATTCC 600  
AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTTGGTG CTGCATATCC CCTACAATAA TTAAACCTTT TTTCTTATTT AAAATGTGTC 60  
50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120  
ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAAATGAA 180

CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300  
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGC GCCT ACAnTTCTTA ATTCAGCGGA 360  
 5 CGGTCACTTG TTAAAACGGT TTAAGGTATT CTACTAATTn 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTTrGTA 60  
 20 tCTCACGCAA tCTTGGTGGT CATTCACTTC GTATATGGCA TCCATTAAGA CGCGAAGATC 120  
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180  
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAATACA GTGTCTCGCT CTGTTTCTGC 240  
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTGCGC 300  
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGga ATCGTATTAG 360  
 30 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420  
 TTCTTGGCAT ATTTCACTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60  
 45 TGTCCAATTG AAACACCTGA GGGACCAAAC ATTGGATTGA TTAATCATT ATCAAGTTAT 120  
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180  
 50 CATGCTATCA CTGATCAAAT TGACTATTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240  
 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTCGTTTCA TGGATGATGA AGTTGTATGT 300  
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAAA TGGATTATAT GGATGTATCG 360

## (2) INFORMATION FOR SEQ ID NO: 3768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTTAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT 60  
 ATGCCTGGCA ACGTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG 120  
 CTTAACTTCT GTGTTCCGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT 180  
 ATGAATGTAA TTTATACATT CAAAACCTAGA TAGTAAGTAA AAGTGATTTT GCTTCGCAAA 240  
 ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG 300  
 CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG 360  
 AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT 60  
 CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA 120  
 ATCTTTCTnC TGCACTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA 180  
 CGTTACCAGC AATAATTTCa TTTTGTGCTT CTTCAAAAGG TGCTTTGACA ATGACCGTAC 240  
 CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAGC 300  
 CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTTCGTATA AACATTAATT 360  
 GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TTAAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60  
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120  
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180  
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240  
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300  
 AGTGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360  
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60  
 30 GGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120  
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180  
 GCTTGTTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240  
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300  
 TGCCTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360  
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTG 400

## (2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

50 TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC GGTCTCAATG CGGCTCATCG 60

55

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180  
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240  
 5 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTGCTTT TTATTTTGAC GTTTTAGACA 300  
 TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCTGGGCA 360  
 ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3773:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60  
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120  
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTCACAC 180  
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240  
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300  
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360  
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

(2) INFORMATION FOR SEQ ID NO: 3774:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60  
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 120  
 50 CTTTCCTCTC CTTGCGCTCT CACTTACTCA TTTAGCTCTA CTAACTCGT TCGGTTCTTT 180  
 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240  
 TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAA TCGGCTCAT 300

GACGCTAAGG AGCTTAAACT TCTGTGTTTC GGCATGGGGA

400

(2) INFORMATION FOR SEQ ID NO: 3775:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC 60

TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT 120

TGCTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA 180

TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAAACA CGTGAACGGC TCAAATGGAA 240

GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC 300

CAAACATTGG ATTGATTAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA 360

TTGAAACACC ATATCGTAAA AGTTGATTTG GntACACAGC 400

(2) INFORMATION FOR SEQ ID NO: 3776:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 60

TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA 120

GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 180

CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 240

AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACHTAG GCGATTATTT CTTATGGAAT 300

TCAAGCTTAT TTAAGACTCT TTATTCATC GGTTCCTTGCCT GGTAAATC TAnATTTTAC 360

TTACnTATCT AGGTTTTTCAA TGTACAAATA ATGGTGGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3777:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TGC GTGACAG 60  
GCAGGCGTGT TAACnCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 120  
ACCCCGCGGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG 180  
GGTATTCTTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG 240  
15 AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT 300  
AGTGGCGGTG GAGGGGATCG AACCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA 360  
GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 400

20

(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGTC AGTCATAGTG CCGTCAGCTT 60  
TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT 120  
35 CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA 180  
CTTGTATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT 240  
GaTGACTTCT GACAGCATAA GCATCTTGaT CTTGCGGTGA TACGTCAAAT TGGGATGCTA 300  
40 CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCaA TTGTAAGGTT 360  
GGATTGTTTG TGGGCTTCGT TnGCCACnn TTGGTACGGC 400

45

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:



CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120  
 CTCGGTTGAA ACCTTACTTA TTCATTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180  
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240  
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTTCGAT GTATCATTTG GGTTTAGCAA 300  
 ACAGCCATAA CCTTCGTCAT ATAAATGTTC ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360  
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

## (2) INFORMATION FOR SEQ ID NO: 3780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGCACACn CAGGCGTGTT 60  
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTGAA CCCCCGCGAG 120  
 CCGTTAAGCC CCGTTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180  
 AAAATTATAT GGACCTTGCA GGA CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240  
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300  
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTAGC CTCTAGCCAG CTGAGCTACA 360  
 35 CCGCCTTATA TAGTTTGTA ATAATATGGT GGAGACTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60  
 TCTAGCACGT TCATAAATAG TTA CTGATA TCCTAGTAGA TTAAGTTCTT CAGCAGCAGC 120  
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTTC TCTCTACGGC GACTCGGAAC 180  
 TTTGCGCGCT ACCCAACCAT TTTCAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTCGCTT AAGCGTCATA AGCAGTTTTA 360  
 AAATCTTGAT GATACACCAA GTCGTCCanT CAGGATGGAG 400

5 (2) INFORMATION FOR SEQ ID NO: 3782:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60  
 CATTGATAAA TCGCTTGAAA TGTTGCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120  
 20 TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180  
 ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240  
 CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300  
 25 AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAAGATGC CATTGCCTAA 360  
 ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

40 AATCGGGTGA TGTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60  
 TGGATAACTG TTTTAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120  
 TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180  
 45 CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAT TAAATCGCTG TTGTCCACAT 240  
 AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300  
 CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGanTT 360  
 50 ACAAATCTT CnAAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTACTAAGA TGTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60  
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCCGA AATCTCTGGA TCAAAGCTTA 120  
 CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240  
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300  
 TTTAAAATAA TTAACTCAT TGTCTGCAAA ACGTTTTCTT TTATAAAAAG AATTTAAACG 360  
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnGA 400

## (2) INFORMATION FOR SEQ ID NO: 3785:

- (i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60  
 35 CCAAGTATCG CCTTgncGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120  
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180  
 TTTCGCAATT TGTTCCTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240  
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300  
 CTGAAATAGT TGA CTAGGCA TTTTGGCGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360  
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3786:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60  
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120  
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTACTAG 180  
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTTAC GACGTGTTAC 240  
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCGCC ATAATACCTT TTTCAACCAC 300  
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360  
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3787:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

25 TCTCTTCCCG TTTCGCTCGC CGCTACTAAG GGAATCGAAN TTTCTTTCTC TTCCTCCGGG 60  
 TACTAAGATG TTTCAGTTCT CCGGGTGTGC CTTCTGATAT GCTATGTATT CACATATCGA 120  
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTTCGGAAA TCTCTGGATC AAAGCTTACT 180  
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240  
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 300  
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTTAAACG CGTTATTAAT CTTGTGAGTG 360  
 35 TTCTTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGAATA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60  
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120  
 TTTTGATGA TTCTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTC 180

TCTTCTGCAA ACAACAACT ATTTTATTA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300  
 CTAGCTGCTA AnACATTATA ATCAGCTGGA TGTTGATGCT TTAACCTCTC TGTTTTAGCT 360  
 5 AATGGAGATT TTAAACGATC TACATTGAC TCTTCATAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3789:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60  
 20 AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120  
 CGGTGTTTTT GGCGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180  
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTG TCCCTATTGT 240  
 25 CACAGCATTT GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTGGC CAAGCATACA 300  
 nGCCGGCATT TATCATGTTG GTGGGATTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360  
 TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3790:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60  
 TTAAATTAT ATACCCACCA CATTTGGTGA kGAACCTAAA AAAAAGCACT TCCCAAAAAT 120  
 45 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180  
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGC TAGCTGGATT CGAACCAACG 240  
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300  
 50 AGGGGGGCAG ATTGCAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360  
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

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CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG COGTGAAAGG GCGTGnTCTT 540  
 AACCGtTGAC CAAGGAGCCA TGGCTCaCcA GGTAgGACTC GAACCTACGA CCGATCGGTT 600  
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660  
 CTACTCTAGC GGAACTAAAG TtnGAACTna CCATCGACGC TAAAGGAGCT TAACTT 716

(2) INFORMATION FOR SEQ ID NO: 3791:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

20 TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTTA AAGGTAACAC TATCATTAT 60  
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120  
 ACGTGACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180  
 25 AACAGCACAT CAGCTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240  
 AATTAATGAG GATTTGGAAA CATTCCTTTC nTGATTTTCA AACATTAGCT GTGATCGGTA 300  
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360  
 30 CTTATGTCGT TGTTAAAACA AATTTTGAAA AAAGGAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3792:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60  
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120  
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180  
 TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240  
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAATT TTGTCATGAT GTGCCTCCTT 300  
 ACGGTATGAT GTtATTCAAA GTAAATTGCT TTGCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA

425

## (2) INFORMATION FOR SEQ ID NO: 3793:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 60  
 AGTGACGGAG nAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG 120  
 GAGGGGGGCA GATTGAACT GCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA 180  
 GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTAAAT AATCAAAATG GTGGAGAATG 240  
 ACGGGTTCGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT 300  
 CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTTA CCGCCGTGAA AGGGCGGTGT 360  
 CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG 400

## (2) INFORMATION FOR SEQ ID NO: 3794:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC 60  
 TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA 120  
 TGTnTCACAA CGTTACCATT ACGTTTAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA 180  
 CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT 240  
 GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA 300  
 GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC 360  
 CACATTCGGT TTATTCATAG CGGACCAGTT TGCCTCCATT 400

## (2) INFORMATION FOR SEQ ID NO: 3795:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

	GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA	60
10	TGGTAGGAGA GCGTTCTAAG GCGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG	120
	AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT	180
	AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC	240
15	AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTAAATCGAT	300
	GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTGATTG CACGTCTAAA GCAGTAAAGC	360
20	TGAGTATTAG GCnAATCCGG TACTCGTThA AGGCTGAACT	400

(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

	GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA	60
	ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG	120
35	CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA	180
	AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTCACTAC	240
40	TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC	300
	AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC	360
	AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT	400

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(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
50	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:



5 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG ACGCTGATGT GCGAAACGTG 120  
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180  
 TAGGGGGTTT CCGCCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240  
 CGACCGCAAG TTGAAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300  
 10 GTTTAATTCG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACACTCTAG 360  
 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

## (2) INFORMATION FOR SEQ ID NO: 3798:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

25 CACAAAACAA GCCAAGCAAA ACAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60  
 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120  
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180  
 30 AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TGCACATAT GGGCCTAGAG 240  
 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAAA CATTACGTAT 300  
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360  
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

## (2) INFORMATION FOR SEQ ID NO: 3799:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

50 CTTGCGCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60  
 CGTTACTTGG TTTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120  
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTGATGCA TCAAGTGCCT 180  
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

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TTTtAGTGCG TtACTGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTn TTTTCGGTGC 360

CATTAAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

(2) INFORMATION FOR SEQ ID NO: 3800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAT GTGTTAGGTA AAGGTGTCAT 60

TGTCGTCAAT GATGTGCCTG GCTTTGTGCG AAATAGAGTC GGCACGCAA CAATGAATGA 120

TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180

GCAAGCGATT GGTGCTCCTA AACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240

TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAGTACC TGAAGAAACA CCTTATTTTC 300

ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAnnCGnAA 360

ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GGnAACTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60

TAAATTGTAA AACGATAGTT CCCGTTGTTC CTAATAGTTG TATTCTATCT GACGCATAAT 120

GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180

TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACCTTAA TGTTCAACT AGTTTTTCTG 240

TCGTTAACAT GGGTTCACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300

TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360

TTATnATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTTCAC TTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGCTCCG GTTTC CCGAA 60  
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120  
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCATGT ATTAGGCACG CCGCCAGCGT 180  
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GTCATAAAT 240  
 ACTAAATAAT GTTTGTAAC TATAGTTACG TTTTTTGGAA TTAACGTTGA CATATTGTCA 300  
 TTCAGTTTTT AATGTTTATT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360  
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3803:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 60  
 35 TTTTGCTTCG CAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120  
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180  
 40 AACCGAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240  
 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300  
 TATGTCCATC CCGTCTCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360  
 45 ACGGATAGGG ACCGAACTGT TTTACGACG GTnCTGAACC 400

## (2) INFORMATION FOR SEQ ID NO: 3804:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 457 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGCCTCTGCC AGTTCGCCA CCCCggCACT 60  
 ATAAAAATGG AGCAGAAGAC GGGATTGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120  
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180  
 TTAGwATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240  
 GAGGATTGGA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300  
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCAAC CTACTGATTA CAAGTCAGTT 360  
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420  
 15 TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

## (2) INFORMATION FOR SEQ ID NO: 3805:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTATT TTGACGTTTT AGACATAAAA AAAGCTCAG GTCTCAACTT GCCTGGCAAC 60  
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT 120  
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240  
 35 TTCTTTGTGT TTACTTTTTA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300  
 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGGCAACGT TCTACTCTTA GCGGAACGTA 360  
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGGACTGTG 400

## 40 (2) INFORMATION FOR SEQ ID NO: 3806:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60  
 TTTACTGAGT CATTGCACTT ATCATAACA TTATATTTAG CATGAGTTAT ATTACTAAAA 120

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TCATTGGCTT AATATTTACA GCGCTTGGA TTGCAGGTGC CGTATTACCT TTTACTGCCAA 240  
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTTGCTCG AAGTTCAGAT CGCTTTTACA 300  
 5 ATTGGGCnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360  
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3807:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60  
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGAAC TA TTCGTCTATT AAAAGCGATG 120  
 TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180  
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240  
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTCGTG CAAGTTATGG 300  
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360  
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

## (2) INFORMATION FOR SEQ ID NO: 3808:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

ATGCGCAGAG TATATGGAGG AACACCACTG TCGAAGCGCA CTTTCTGGTC TGTAAC TGAC 60  
 45 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120  
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180  
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAAC TCA AAGGrATTGA CGGGGACCCG 240  
 50 CAcAAGCGTG GGAGCATGTG GtTTAATT CG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300  
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCCTTAAGC TTATTTGCCA TCATTAA

447

## (2) INFORMATION FOR SEQ ID NO: 3809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

CCAACCTGAGC TACTGAACCA TAATAAAAAT GTAATGACTG GCGGTCTCGA CGGGAATCGA 60  
 ACCCGCGATC TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCTATAAA 120  
 ATATTGCGGG AGGCGGATTT GAACCACCGA CCTTCGGGTT ATGAGCCCGA CGAGCTACCG 180  
 AACTGCTCCA TCCCGCGATA ATAAAAATA ATGGCGGAGG AAGAGGGATT CGAACCCCCG 240  
 CGGCCCCGTTA AGGCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCCGAC TTGGGTATTC 300  
 CTCCATTATT ATAGGTAAAT CGCTATTAAT TATAAAATTA AATGGCGGTC TCGACGGGAA 360  
 TCGAACCCGC GATCTCCTGC GTGACAGGCA GCGGTGTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3810:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA ATAATGGTGG 60  
 GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA 120  
 GCTATAGGCC CATTTTTTTG AATGTTAAAT AAACATTCAA AACTGAATAC AATATGTCAC 180  
 GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG AGGTGATCCA 240  
 GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT GTCCACCTT 300  
 CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC TCTCGTGGTG 360  
 TGACGGGCGG TGTGTACAAG ACCCGGGAAC GATTTCACCG 400

## (2) INFORMATION FOR SEQ ID NO: 3811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

	GCTTCATGCT TAGATGCTTT CAGCACTTAT CCCGTCCACA CATAGCTACC CAGCTATGCC	60
10	GTGGGCACGA CAACTGGTAC ACCAGAGGTA TGTCCATCCC GGTCCTCTCG TACTAAGGAC	120
	AGCTCCTCTC AAATTTCTTA CGCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC	180
	TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCCTGGG ACCGACTACA	240
15	GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGGAATCT	300
	TGGGGGAGAT AAGCCTGTTA TnCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC	360
20	ATGCGGGAAC CACCGGGATT	380

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

	GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG	60
	CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAACCTG	120
35	GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT	180
	CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCAGCAG GTTCTGAACC CAGCTCGCGT	240
	ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA	300
40	GCCGACATCG AGGTGCCAAA CCTCCCGTC GntGTGAACT CTTGGGGGAG ATAAGCTGTT	360
	ATCCCCGGGT GAGnTTTnTC CGTTGA	386

(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

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CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTTGGTAC TTCTGGTGTC 120  
 GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180  
 5 TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240  
 AATTGATAAC TTGGTTTATC TTTATTGTGA TCTTCTTCAA TAATTTTCAGT GTGCTTATTG 300  
 AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360  
 10 TACTTAGGTT TGTCTTTTTC TGTAnCTTCC TCGAATGACT 400

(2) INFORMATION FOR SEQ ID NO: 3814:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 25 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCnACTA AACTCGTTGC GCnCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GCTCATCGCA 240  
 30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300  
 CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360  
 35 TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3815:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

TTCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60  
 GAATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120  
 50 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180  
 CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTAA AGCGATATAT TGATGTCTAG 240



GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360  
 TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60  
 GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120  
 TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACCT CGCCAAGCCA TCTTTCTTTG 180  
 TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240  
 CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360  
 GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTTATTGTT CAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60  
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120  
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180  
 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240  
 TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300  
 TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360  
 GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60  
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120  
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180  
 15 CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240  
 TTCTGAATAG GCGCTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300  
 CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360  
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCCAATCGAA 400

(2) INFORMATION FOR SEQ ID NO: 3819:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAG TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60  
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120  
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180  
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240  
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300  
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TGCGAGACCT 360  
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3820:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TGGCTCGAAC CACCGACCTC ACGCTTATCA GGCCTCGCTC TAACCAGCTG AGCTATAGGC 60  
 CATTAAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120  
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180  
 ATACGGCTAC CTTGTTACGA CTTACCCCA ATCATTGTGTC CCACCTTCGA CGGCTAGCTC 240  
 10 CTAAAAGGTT ACTCCACCGG CTTGCGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300  
 GTACAAGACC CGGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360  
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

15 (2) INFORMATION FOR SEQ ID NO: 3821:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

25 TATTAAATTA ATGGTGGGCC TAAnTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60  
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120  
 30 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180  
 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240  
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTAC 300  
 35 AAATCTCTGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360  
 GCTGATCTAC GATTACTnAG CnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

50 TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTGGAAC CAACGAGTGA 60  
 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120  
 GCAGATTGGA ACTGCCGAAC CCGAAGAGCG GATTTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300  
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCCG 360  
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAATAA 400

## (2) INFORMATION FOR SEQ ID NO: 3823:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60  
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120  
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCGTGTTT AATCATAGTA AGCAAATCAT 180  
 GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240  
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300  
 TCTCATGTTT TCGAGATCCA CCAAATGTnA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360  
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

## (2) INFORMATION FOR SEQ ID NO: 3824:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60  
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180  
 ACGCGTTATT AATCTTGTTG AGTGTCTTT CGAACACTGA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 50 ACnTATCTAG TTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360  
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60  
 TTACTIONACAG CTCCCCAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120  
 CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180  
 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240  
 TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATnTT ACTTACTTAT 300  
 CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360  
 CCAAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60  
 AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120  
 ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180  
 TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240  
 GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300  
 TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360  
 CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

	AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTAG AGAAGACCAA AAGAAGAAAA	60
5	GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AACAGAGAA AATATAAAGA	120
	AATGGTTTGG AAATGCTTGG GACGGCGTAA AACTAAAAC TGGTGAAGCC TTTAGTAAAA	180
	TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG	240
10	GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA	300
	CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGGG AAAGCTTGGC CAATCTGTTA	360
15	AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCCAA	400

(2) INFORMATION FOR SEQ ID NO: 3828:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 400 base pairs |
| 20 | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

	TCTCAGTTCC AGTGTTGCCG ATCACCCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA	60
	GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC	120
30	GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG	180
	AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA	240
35	TCAGAGAAGC AAGCTTCTCG TCCGTTGCTG CACTTGTCAT GTATTAGGCA CGCCGCCAGC	300
	GTTCATCCTG AGCCAGGATC AACTCTCCA TAAAAATTAT GATGTTGANT AGCTCATAAA	360
	TACTAAATAA TGTGTAACT TATAGTACGT TTTTnGAAAT	400

(2) INFORMATION FOR SEQ ID NO: 3829:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 400 base pairs |
| 45 | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

50	CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA	60
	GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAAAT	120

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ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240  
TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTGCGATT 300  
5 CAAGTGGGAR sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360  
ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTC 400

(2) INFORMATION FOR SEQ ID NO: 3830:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

20 GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60  
CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120  
ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
25 GGATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTA TAAGTCAAAC 240  
GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAATCTGCT 300  
TTAAAATAAT TTAATCAIT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360  
30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

- (i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG 60  
45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTA CAATCGCTTG CTTCTTTCCT 120  
CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTA CTAACT CGTTGCGCTC TTTTCTCGTT 180  
TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240  
50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300  
TTTTTTGCCT GGGCAACGTT CTA CTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

## (2) INFORMATION FOR SEQ ID NO: 3832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCACCTC TGGTTTTGCT TGGTAAAATC TATATTTTAC 60  
 TTACTTATCT AGTTTTCAAT GTACAATTTT TTTTTAGTCA AGCGCTCGCA TAAGCAATAT 120  
 CACTTTAACC AAAAAATATT TGAATGTTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180  
 ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240  
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 300  
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360  
 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA 400

## (2) INFORMATION FOR SEQ ID NO: 3833:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT 60  
 TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCCAT ATCATGCAAT 120  
 TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT 180  
 AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTCATA ATGTGTTAAA 240  
 TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATnT ACGGGTTACC 300  
 AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTnAA 360  
 AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3834:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5    nAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC       60  
       TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA       120  
       GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC       180  
 10    CGCCTTATAT AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC       240  
       TGCGTGCAAA GCAGGCGCTC TCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC       300  
       GGGAAGACAG GATTCTGAACC TGCGACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG       360  
 15    AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA                               400

## (2) INFORMATION FOR SEQ ID NO: 3835:

## (i) SEQUENCE CHARACTERISTICS:

- 20       (A) LENGTH: 400 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: double  
        (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

      AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT       60  
 30    CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA       120  
       AGGCGGAGGA ATCACATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT       180  
       AAAAAATTAT GGTGATTGTC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT       240  
 35    AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT       300  
       GCAGATGCCT TGTCAGGTGA AGACATCACG TATCnAGAAG CGTGCGCAGA TGAAGAATAT       360  
 40    CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG                               400

## (2) INFORMATION FOR SEQ ID NO: 3836:

## (i) SEQUENCE CHARACTERISTICS:

- 45       (A) LENGTH: 400 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: double  
        (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

      CTAATCGCAT CTTTTTCAAT CTAAGTGCCT TTGTGACAAA CTTACTGAAC TTAGTGCCAT       60

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180  
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240  
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300  
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360  
 10 CAATTGTGGC AGCTTTTThC TTCCGGnGAA AATATChGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TAITCATATA 60  
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120  
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180  
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGA CCAAGGAGCC ATGGCTCAAC 240  
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTA CTCTAGC GGAAGTAAn TCGGACTACC 360  
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC 60  
 GTTCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTC 120  
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240  
 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

TCAGATCCAA ACGTTTTTCAn TCGnCCAAGC CAATTTGCCT

400

## (2) INFORMATION FOR SEQ ID NO: 3839:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

15 TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrc GACTCCTCTT 60  
 AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC 120  
 TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC 180  
 20 TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT 240  
 TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC 300  
 TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT 360  
 25 CTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTcAG 416

## (2) INFORMATION FOR SEQ ID NO: 3840:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

40 AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 TCCTCTCCTT CGGCTCTCGC TTACTIONTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 45 TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAAACTTG CCTGGCAACG 240  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 360  
 50 CTCGTTGGnG CTCTTTTCT CGGTTThGTC AGAnTTCAAA 400

## (2) INFORMATION FOR SEQ ID NO: 3841:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

	CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA	60
10	ATTCCTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA	120
	TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG	180
	ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG	240
15	CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT	300
	AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTTG TAGTGGTGAA	360
	GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA	400

20

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

	TCGCGATTCTG CGTGTTGAGA AATCATCGGC ATCGCGTCAT TCAATGATTG ATATGCATCT	60
	AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA	120
35	TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT	180
	CCTTGTTCTGA CATTTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT	240
	GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA	300
40	CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTC	360
	AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

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GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120  
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT 180  
 5 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240  
 GGCCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300  
 10 CTATTTTCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360  
 TCATCCGnTC ACTTTCAACG TAAnTCGGGT CGGGTCTCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3844:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60  
 25 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120  
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC 180  
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240  
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300  
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360  
 35 AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTAT TTTCTGCATT 420  
 TTTAATAGTA TCGTGTTTAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

## (2) INFORMATION FOR SEQ ID NO: 3845:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60  
 50 GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TGCGTAGAGC AATTGCGnAA 120  
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

TTAACATTCT TACCTTATGT TGTTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300  
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360  
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60  
 20 TCTCCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 120  
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180  
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240  
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300  
 AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTACT CATTAGCTC TACTAAACTC 360  
 30 GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAGG TATTACGATG 60  
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120  
 45 GCACGTCCAT TAAGACGTAT TGTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180  
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240  
 50 AAAAGGTAAG TAACGACACT TTAACATATC GCGCATCAAA AATGAGCATC AGGTCGCCCT 300  
 TGCCTGTGGC TCATTTTTTT GAATTATTTT CCTGGGAAAA TGATTCGCTG TGTGCTGTTT 360  
 TGTThCCACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

TTTAAAACTC TTTATTCACT CGGTTTIGCT TGGTAAATC TATATTTTAC TTACTTATCT	60
AGTTTTCAAT GTACAAATAA TGGTGGGCCT AAGTGGAATC GAACCACCGA CCTCAGCCTT	120
ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCATTT TTTTGAATG TTAAATAAAC	180
ATTCAAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA	240
TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTGGTnACG	300
ACTTCACCCC AAATCATTTG TCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC	360
GGCTTCGGGn GTTACAAACT CTCGTGGGTG TGACnGGCGG	400

(2) INFORMATION FOR SEQ ID NO: 3849:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC	60
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT	120
TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT	180
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA	240
AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTTG CCTGGCAACG	300
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT	360
GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3850:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60  
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120  
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180  
 10 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGGAATTTAT TAGGTGTACA AATGACCACC 240  
 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300  
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360  
 15 TCTTTGAGTT TCAGCAATGC TGGAATATGA CCGTCTGTG CAATACCACC AACAACTATG 420  
 CACACCAACT TTTAAntTTG TnCATGATGT GCCnGCTTnA CCG 463

## (2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGATTcG ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60  
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCC 120  
 AACCCGAAGG AGCGGATTTA CAGTCCGcCG CGTTTAGCCA CTTCGCTACC CCTCCAGCTT 180  
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCCTCT 240  
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300  
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360  
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTtAA CAGCCGATAG CTCTACCACT 420  
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480  
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540  
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn 600  
 TTAGTAAGTA AAAGTGGATT TTGGnTTh 628

## (2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCTGAATT GGCCGTGTAG TAGCCGATAT 60  
 ATTTGCCAAT GGTATACAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120  
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180  
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240  
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300  
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360  
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3853:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

25 TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60  
 30 TCATAAGAAA TACTAATTTT TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120  
 TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180  
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTTGCACATT 240  
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACCTG CATTGTCTGT 300  
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CCCCACCTnC GCATTGCCTG 360  
 TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGGCCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3854:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

55

GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180  
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240  
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300  
 TTAAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360  
 CAGTTGCAAA TgNTATTGTC AGCCACGAGT ACGGCTGGTA 400

10 (2) INFORMATION FOR SEQ ID NO: 3855:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60  
 AAATCAACAG GTAAAAAATT AACAAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120  
 25 TTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180  
 GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240  
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300  
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360  
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3856:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60  
 CTATTTCTTC TATTGTAAAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120  
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTGAT TCGTGATTTT 180  
 50 GAATACTTTT CTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240  
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAGTCAA 300

TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

15	GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTTGA	60
	AGTTGTGAAT GCACATGGTA AACATTTTTG TGCATTACCA CGTGAAGATG AAGATATTGC	120
	AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA	180
20	TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT	240
	AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTG TCATTAnATC	300
	TATGATTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCIT GCCGAGTAAT	360
25	TGTCAAATGT ACTATGCAAT G	381

(2) INFORMATION FOR SEQ ID NO: 3858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

	GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG	60
40	ATGAGGTAA TAGGTTGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT	120
	CGATCGAAGA CTTAATCAAA ATAAATGTTT TCGGACAATT CACTTTTACT TACTATCTAG	180
	TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT	240
45	TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC	300
	GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA	360
50	GGnCTnTTTG TTTTTATGT CTAAAACGTC CAAATTAAnA	400

(2) INFORMATION FOR SEQ ID NO: 3859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAT CGTGTCAATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTTAAATC TGTTTAAACA TTATTTTGAA TTTCATTCAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
20	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG AITCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
	TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGnGC	400

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(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60  
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120  
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180  
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAAAC nGTCCAGATT GCGCACTGAT 240  
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300  
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360  
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

## (2) INFORMATION FOR SEQ ID NO: 3862:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

25 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60  
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120  
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180  
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240  
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300  
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360  
 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

## (2) INFORMATION FOR SEQ ID NO: 3863:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

50 TCGGCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAATCGTTG 240  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 300  
 TGTTTGCTTT TTATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG 360  
 10 CGGCTCATCG CATnCATnT TGCCGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60  
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGT TATGGGAAAT GAATTAATGT 120  
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180  
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240  
 30 GAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300  
 GCAATCGAT CCAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360  
 TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATCAAC GCATGTAGTA CCACATCTTC 60  
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120  
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCAGATG 180  
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240  
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

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## (2) INFORMATION FOR SEQ ID NO: 3866:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

15	AAGTCAATAA CTTTTTTTAT CTGTGCCATT TTATTTTTTA ACCAAAATTT GATTAAAAAA	60
	CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA	120
	GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA	180
20	TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA	240
	AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT	300
	GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT	360
25	TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG	400

## (2) INFORMATION FOR SEQ ID NO: 3867:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

	CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA	60
40	TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC	120
	TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTCTTGAT TTCACACTGC CGAGAAAAGC	180
	CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT	240
45	CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG	300
	AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT	360
50	GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA	400

## (2) INFORMATION FOR SEQ ID NO: 3868:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTTGA TCACTGTTTA 60  
10 GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT 120  
GTTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT 180  
GACAATGTTA ACTTTGATTA TCTATTGCC GCAATTGGTG GTGGCGGTTT AATTTCAAGT 240  
15 ATTAGTACTT ACTTTAAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA 300  
GGTGCCAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA 360  
AnTCGATAAA TTTGTGGACG GTG 383

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(2) INFORMATION FOR SEQ ID NO: 3869:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA 60  
CGACAACCAC CACCTGTAC TTTGTCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA 120  
35 GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG 180  
nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTGCTAC TCCCCAGGCG 240  
GAGTGCTTAA TGC GTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC 300  
40 ATCGTTTACG GCGTGGACTA CCAGGGTATC TAATCCTGTT TGATCCCCAC GGTTCGCAC 360  
ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTGCGCAAT 400

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(2) INFORMATION FOR SEQ ID NO: 3870:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:



GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120  
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180  
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240  
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTTCGAA 300  
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360  
 10 GCTTGGTAAA AGCnnGn 377

## (2) INFORMATION FOR SEQ ID NO: 3871:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCCTCCCATG TATATCCTAC CCAACATGA CCATCTTGTA ACATCACTTC 60  
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120  
 CCCCACCTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTA AATCTAGCAC TTTCTTCCAT 180  
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACCTGCA ACTGGTTTAA CTGTATTACT 240  
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300  
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360  
 35 GCGAGTTACn GGGGTCCAAA CCnTGGTGT AAAAnCGAAC 400

## (2) INFORMATION FOR SEQ ID NO: 3872:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60  
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180  
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360  
 CTGCGTGCAA ACGGGCGCTC TTCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 584 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCAG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60  
 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120  
 GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCCTTGCGCT CTTTCTCGTT TCGTCAGATT 180  
 CAAnnGTTTT CAATCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240  
 GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300  
 GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360  
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420  
 TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 480  
 GCCATTTTTC TTTGTGTTTA CTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540  
 TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240  
 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

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(2) INFORMATION FOR SEQ ID NO: 3875:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60  
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120  
 CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180  
 CCGACATCTT TAATTAATTG CTTTGACAGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240  
 GATGGGAATA TCATGTTATC TTCAATCCGT CACCAAACAA GTCACCTTGC TGCATCAAAT 300  
 AACTGATTCG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360  
 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60  
 TGGTGATCCT CAATTCGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCGTCA 120  
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180  
 CGCACGTACA GTGGTTGAAA AAGGTATTAT GGCGGCACTG CACGTnTTGC TCGGAAAAAA 240  
 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300  
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360  
 CCGGGGGGTC TACAAAATCT GGTCGTGACT CTAGACCGCA 400

(2) INFORMATION FOR SEQ ID NO: 3877:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

	ACCAATTTCT CTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC	60
10	CATCATGTTA TGTGATTGGA ATACTTTTTT AAAATCATAT TTAATACCTG GAGGGAATTT	120
	ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT	180
	TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT	240
15	ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACTTCTGG GnGTATCAAA ATGnTGCAAT	300
	GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC	360
	TCAACACCTT AGGGGTTAAC TTCGGCCATA TCCCTTTTGG	400

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(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

	ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCTATTAA CAAAAGAAGA TG TAGATGCA	60
	TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA	120
35	GAAGTTGCTG AAACCTCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA	180
	AACAACTGGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC	240
40	TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG	300
	GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA	360
	CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT	400

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(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

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TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120  
 TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180  
 5 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240  
 CTTGCGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 300  
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTGCTTTT ATTTGACGTT 360  
 10 TAGACATAAA AnAAGAnCCT TCGGnCTCA ATGCGGCCAT 400

## (2) INFORMATION FOR SEQ ID NO: 3880:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60  
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120  
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180  
 GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240  
 30 ATGGATATTG ATTCGAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300  
 CTCTCGGTCA TATTCAGGCA TATCCGACA CAACCTGGAT AGCAGTTGTG ATTTCCCAGG 360  
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60  
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120  
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180  
 TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360  
 ACAGGTAGTC CAAGATGGAG AntCTnAAGG TGGAGCGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3882:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60  
 ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTGGAATT CTCTGTGTTG GGGCCCCTGA 120  
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTT AGTCAACTAC TGCCAATATA 180  
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240  
 ATATTTAATT TGC GTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300  
 TAAGTTTCA GAAATAAACC TATCTTAAAA TATAAAAAAA TCGAGAATTC GTAGTTTAAT 360  
 AACGAAATTC TCGTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420  
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACATAA 480  
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540  
 AGATTCATAA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600  
 CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60  
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120  
 TTATTTGTTG TTACGTGGAC TTAACACTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180  
 CGCTAGAAAA CTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

GAAAATTTAG ACATTTCaT TTTTGCAGAA AGTTTAGGAg GTACkGAAAC ATTAGTGACC 360

TTCCCTTACA CCCAAACACT GTTGATATGC CAGT 394

5 (2) INFORMATION FOR SEQ ID NO: 3884:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60

TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120

20 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGATTAG CGTAACAAAA TATGGACCTG 180

TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240

ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300

25 CAATAACGAC GCCAACACTA AAAAnTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360

AAAGAGGAAT CACAAAAGTT CCnTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

40 TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCITTATTCA CTCGGTTTTG 60

CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCa ATGTACAAAT AATGGTGGGC 120

CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGGCTCTAA CCAGCTGAGC 180

45 TATAGGCCCA TTTTTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240

TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300

50 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360

GACGGCTAGC TCCCAAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

55

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60  
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCAATTGGA AACTGGAATn 120  
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180  
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240  
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300  
 20 GTTAGGGGGT TTCCGCCCCT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360  
 GAGTTACGAC CGCAAAGTTT GGAACTCAA AGGGAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3887:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

35 ATTTTTTAAT TTTTCATGCAA ATTTTTAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60  
 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACTAGT CGAAAATAAA 120  
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180  
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240  
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 300  
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAACT 360  
 45 TACACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

## (2) INFORMATION FOR SEQ ID NO: 3888:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



EP 0 786 519 A2

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAAGCTG GAACTTACAA 60  
 GTCTAGTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120  
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTCGATTCA TAAAATTAAA 180  
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240  
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTACACA GCTTCATTAA TAAAACGACT 300  
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360  
 AACGAATCCG CTTCATCCAA AATCAnCCAT TCTAACGCAC 400

(2) INFORMATION FOR SEQ ID NO: 3889:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGChAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aAAGCAAGGC 60  
 GCATTATTC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120  
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180  
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240  
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300  
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360  
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420  
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTTnAAnt GCTGGAAAAT GTTAGCCTnC 480  
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTA CTCTAGC GGAATGAAT TCGGACTACC 240  
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300  
 ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360  
 10 GGTTTTGCnT CGCAAAACAT TTATTTTGn 389

## (2) INFORMATION FOR SEQ ID NO: 3891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60  
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120  
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180  
 TCTAGTGCCT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTGGAACC 240  
 30 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300  
 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360  
 ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60  
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGTTATAAT CGAGGATGAT GTATTAATCG 120  
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180  
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240  
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACCnTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

(2) INFORMATION FOR SEQ ID NO: 3893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT 60

GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAAGTTGCT 120

GCTCCAGTTT CTCACATTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT 180

TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTTGTAGAT 240

CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TTTATTCTG AAGCTGAATT CAGAGATTAT 300

TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAAATGGG TGCCAGAAGG TCATTAAAAG 360

ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAAC TnA 400

(2) INFORMATION FOR SEQ ID NO: 3894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCTTG 60

ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT 120

TAGTACGTGT ATATATCGTT CAAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC 180

GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTGA AGAAGATATG CCTTACTTAC 240

CAGATGGACG TCCGATCGAT ATCATGTAA ATCCTCTTGG TGTACCATCT CGTATGAACA 300

TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG 360

cATCACCAGT ATTTGaCGGT GcAaACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG 420

GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCCnTCCGA 480

TAACC 485

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 507 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

10	GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTCTCT	60
	AGATTGTGGT TTTTLAGTTG GTGCCACTGc TTTAACCTTT TCATTGATTT CAATAACAGG	120
	TGTTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG	180
15	TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCtGGTGTT GCGGGTGTTG GAGTTTCTGG	240
	CTCACTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTCCT GGCTCACTTG GTACTTCTGG	300
20	TGTTGGTGGc GTTGGTGGTT CCGGCTCACT TGGTACTTCT GGTGTGGTG GCGTTGGtGG	360
	CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTGA CCTTCATTTT GGGCCGCTTA	420
	CTTTTGGGAA GTGTATCTTC TTCAAAGTCA ACACIAATGT GGTCCACCGG AATTGATAAC	480
25	TGGGGTTAAC CTTAAATTGG AACCTCC	507

(2) INFORMATION FOR SEQ ID NO: 3896:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

	CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGGnGACTTG TGACAATCGC	60
40	TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG	120
	CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG	180
	TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG	240
45	CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC	300
	CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG	360
50	GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC	400

(2) INFORMATION FOR SEQ ID NO: 3897:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

	TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT	60
10	CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC	120
	ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAAC TTC TAAATTGGGT	180
	CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA	240
15	CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC	300
	AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TGC GCACATG CTCCTATCAA	360
20	ATGGTGTGGG CAATGGTCAA CGGGTGCCT TGGTGTACAG	400

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

	GAAATCACTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT	60
	GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA	120
35	TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATT TG ATGAGGACTT AGCAACACGG	180
	GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA	240
	TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATT TA ATGGCAAATG	300
40	ACAAAAATGG TGTTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG	360
	ATGTCGCGTC ATTTAAAGGA AGCGATTAC CATCGnGATC	400

45

(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

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CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 180  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240  
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300  
 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360  
 10 TTCTTGACT TGTGGACAAT CGGCTTGGCA nTCTTTnCTC 400

## (2) INFORMATION FOR SEQ ID NO: 3900:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60  
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120  
 TAATGTTATT TGTTCAATTCA CTTTCATTCC AACATACCA TCACATCCTC ATTCATTTTT 180  
 CATATAATTC TGTAATATTA CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240  
 30 TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTTC TTTTCGAAAT TCTCTATGTT 300  
 GGGGCCCGCn AACTTGCAAT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360  
 CATCCCCAAC TGCACATTA ATnGCAAGCn GACTTTCCGT 400

## (2) INFORMATION FOR SEQ ID NO: 3901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGCTTCA CTTATACTTC TAGTCACAGA 60  
 TTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CAACTCAAT GCGGCTCATC 120  
 50 GCATTCAATT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180  
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTTCTTGGT GGTTTACCTT TTAATTTGGA CGGTTTAGAC 360  
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCTGCAGA TTCAAACGTT TCACTTCGC CAAGCCATT 240  
 TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300  
 TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360  
 AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAACCATT AATAGATTTT TATTGGTGA TTTCAAATCA TGAGACTGGG 60  
 ACAGAAATGA TGTTTTATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTTTGATG 120  
 AACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180  
 TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240  
 ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATT ACAATTATAA GCGATAATCT 300  
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360  
 CTTTTTAGGT GGGTTTAGGG AATTTCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10 CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60  
 TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG 120  
 CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180  
 15 AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240  
 ATAGCATATC AGAAGGCACA CCCGGAGANC TGAAACATCT TAGTACCCGG AGGAAGAGAA 300  
 AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCAA CCAnCAAGCT 360  
 20 TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA 400

## (2) INFORMATION FOR SEQ ID NO: 3905:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60  
 35 TGgTAAATGA ACAAATCATT GATATTTTCA GTCCGTTAAA GGGCGAAATA GAAGTGCCGG 120  
 GCGATAAGTC AATGACACAC CGTGCAATCA TGTTGGCGTC GCTAGCTGAA GGTGTATCTA 180  
 CTATATATAA GCCACTACTT GCGGAaTtCG TCGTACgATG GaCATTTTCC gACTGTTAGG 240  
 40 TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300  
 TAACACGCCA CATCAAGTnT TGtnTACAGG TAATTCCGGG TACGACAACA CGATTGATAG 360  
 TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

## (2) INFORMATION FOR SEQ ID NO: 3906:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTcAGCAGT AGAAGAGGGA 60  
 ACATTCTAAA CTAAATTTGC TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120  
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTc AAAAAATGATA AAATCGACTT TATTTGGAGT 180  
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAGTGG GTTCTGTGAC ATTAACGTCT 240  
 10 ACAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300  
 AACCATTAAc AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360  
 AAAGGTGGAT TGGCCAC 377

15 (2) INFORMATION FOR SEQ ID NO: 3907:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

AATTAGGTAA TTCAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60  
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120  
 GGTCTCGTAG TGTAGCGrTT AACACGCCTG CCTGTCACGC AGAGATCGCG GGTTCGATTc 180  
 30 CCGTCGAGAC CGCCATTATT ATTACCATTa CGGTTcAGTA GCTCAGTTGG TAGAGCAATG 240  
 GATTGAAGCT CCATGTGTCG GCAGTTCGAC TCTGTCCTGa ACCATTCTTA ATTCATGGCG 300  
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTcGAGGG TTCGATCCCC 360  
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420  
 TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTC 480  
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

55

TAAGTATCAT ATTGTCCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180  
 AAAAGATATA GGGATTATAT TGCCTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240  
 5 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300  
 TATCATCATT TGTTGGGCTA TTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360  
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

10 (2) INFORMATION FOR SEQ ID NO: 3909:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAATGC GGTATATTCA 60  
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120  
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180  
 GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240  
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300  
 30 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCnGTTCCCT AAAATTAATC CAGGGCTTAA 360  
 CATTGCGAGT CCAGGTATTG GntCCAAGCT AATGGGGCCG 400

35 (2) INFORMATION FOR SEQ ID NO: 3910:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

45 TTACCCGATA TCGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60  
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120  
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180  
 50 CTGTAGTTGG TGACGTTATT GTTAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240  
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAAAG

400

## (2) INFORMATION FOR SEQ ID NO: 3911:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTA~~n~~CTC AAGTTATGGG TCCTGTAATT GATGTTGAT TTGAACATAA CGAATTCCTA 60  
 AAATTAATAA CGCCTTGGTT ATTGATGTGC CTAAGAAGA AGGTACAATA CAACTAACAT 120  
 TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTCTGAC AATTGCGATG GATTCAACTG 180  
 ATGGTGTCCA AAGAGGCATG GATGTAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240  
 GTGACGAAAC ATTAGGTCGT GTATTTAATG TACTAGGTGA AACAATTGAC CTAAAGAAG 300  
 AAATTAGTGA TTCTGTTGCG CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360  
 AACTTTTCAA CAGAAGTTCC AAATTTTTAG G~~n~~ACAGGGTA 400

25

## (2) INFORMATION FOR SEQ ID NO: 3912:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAAA TCAACACAAC CAAAAGGTAG AAAATTCAA GATTTCACTA 60  
 GTAAATTTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120  
 CAAATCCTAA TGGAAATAAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180  
 ATGGGAATAT AGTGTCATCG GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240  
 TAAATAGTAA ACACGA~~n~~GCT ATTGGTGTA TCTATGCCG TAATAAGCCA TCAGGTGAAA 300  
 GCACCAGAGG GATTTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360  
 TTTAGATAAA T~~n~~ATTAAGAC CT~~n~~AGACATT CACCCAATCC 400

50

## (2) INFORMATION FOR SEQ ID NO: 3913:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

	ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT	60
10	TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTTA TTTTGACGTT TTAGACATAA	120
	AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT	180
	TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGACTTGTGA	240
15	CAATCGCTTG CTTCTTTCCT CTTCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT	300
	CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT	360
	CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA	400

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(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

30	TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT	60
	CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTTAAT	120
35	GCCAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT	180
	CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT	240
	TCGGTCTAGT TGCTAAATAA TCITTAGCTA ATTGAATTGC TGGTGTGCA GCATAACAAG	300
40	CTTCTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTTG	360
	nACAGCGGCT GCTTTACGAA TTCCAACGTC TGATTCCAGT	400

45

(2) INFORMATION FOR SEQ ID NO: 3915:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

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TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120  
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180  
 5 TCGAAATTGA ACGAnAATTC AAAAACATTA TATCGTGACT TAGTTGAAGA AAAAATAATA 240  
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300  
 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360  
 10 ATTAGAAACA G 371

## (2) INFORMATION FOR SEQ ID NO: 3916:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAAATAGC 60  
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120  
 TATCGTTTGA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180  
 GACTAATAGT AAAAAAGTTA ATCACAAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240  
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300  
 AGAGCTTGAT TTAAATTGA GAAAACAACT TATTGAAAAA CAGATCTTTA CGGTAACATG 360  
 35 GGTTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

## (2) INFORMATION FOR SEQ ID NO: 3917:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 412 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCCnTGAAG GAATAACAaC CTTTAGACCT 60  
 GGAGATTGAG CTAAATATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120  
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180  
 GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

55

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTTG TAGTCCTTCA 360  
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60  
 TCGGGTCAAC GCCTACTGCC TTAAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120  
 CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180  
 ATGTTCTGTC AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240  
 CCATCGTGGT GTCAGGGCGT ATnAAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300  
 GGTCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360  
 CCGACCATCA CCGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60  
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAACTG 120  
 CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180  
 GTAAACTGC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240  
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300  
 ATCGTGGTGC TTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnc TTCACAAATG 360  
 CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10 CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG 60  
 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120  
 ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180  
 15 ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240  
 CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300  
 GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360  
 20 GTCCGTCITT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3921:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTGT 60  
 35 TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAAATT GCTAGTTGGT GATGAGTTTA 120  
 AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT 180  
 CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240  
 40 ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300  
 GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360  
 45 TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3922:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60  
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120  
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180  
 CAATCATTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC GGCTTCGGGT 240  
 10 GTTACAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300  
 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360  
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTTGn 400

(2) INFORMATION FOR SEQ ID NO: 3923:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60  
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120  
 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGCCACT 180  
 30 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240  
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300  
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360  
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60  
 50 CTTCAAACCTA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120  
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCCG CACTGATTCC 180



GCTATTAGCA TGGCTGTCCC TGCTGTTCCCT ATCATATAAA TGATAGATTC AAATAGATTT 300  
 GTAGGGTTGT CATGCCCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360  
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AAnTCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTG AACCACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60  
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120  
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTGCTACC CCTCCAGCTT ATTCATATAA 180  
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCTCT GCTTGTAAAG 240  
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300  
 GTGTTACCGC CGTGaAAGGG CGTgtgCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360  
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420  
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAAnTGAAT TCGGACTGAC 480  
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60  
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120  
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180  
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240  
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

400

(2) INFORMATION FOR SEQ ID NO: 3927:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

15	TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT	60
	GGTTGCATTT AGCGCAACAT GACCATAGTT TTAATAAGC ACAGCGCGCA AGTGATTAAA	120
	GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT	180
20	CAGGAAGACT ACCAAGCTTA TGTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT	240
	ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT	300
	GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGGG TGAGTTTAAG TCCATCGCTA	360
25	AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAT	400

(2) INFORMATION FOR SEQ ID NO: 3928:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

40	GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTGTGC	60
	AnTTTGTAA ATATAGGCCG TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA	120
	GTAATACATC TCCAACATTT GCCTTTAATT CTTTGGCGAT GACTACCGGT CCTGGATGTG	180
	GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA	240
45	CTGAAACATT TGCGCGTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA	300
	CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA	360
50	CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG	400

(2) INFORMATION FOR SEQ ID NO: 3929:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

	CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTAAA CGCTGTTATC TTTATGCCAG	60
10	TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG	120
	TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG	180
	AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGGTA	240
15	CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA	300
	TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT	360
	ATTCACCTAC CACGnAAATT ATAGGTGTTG AACCCnAGT	400

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(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

	ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT	60
	CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCCAAATGA TACATCGAAT	120
35	GGCACATATC ATTGCTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT	180
	GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA	240
	AAAAATAAAT GAATAAGTAA GGTTTCAACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT	300
40	TGTCGTTGTG CCAAATTTGA ACGnTTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT	360
	ATTATTTCCA TGA	374

45

(2) INFORMATION FOR SEQ ID NO: 3931:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

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TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120  
 TTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180  
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240  
 GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300  
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTTAAATGC 360  
 10 CATTAATTA CTAGGTGTTT CCnTAnC 387

## (2) INFORMATION FOR SEQ ID NO: 3932:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAATGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG 60  
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120  
 TGACCGATAG TGAACCACTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180  
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240  
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300  
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360  
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

## (2) INFORMATION FOR SEQ ID NO: 3933:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GACTACATG 120  
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360  
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60  
 CTTTTGCGCT GGCAACGTTT TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120  
 AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180  
 ATATGAATGT AAATTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240  
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300  
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360  
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

(i) SEQUENCE CHARACTERISTICS:

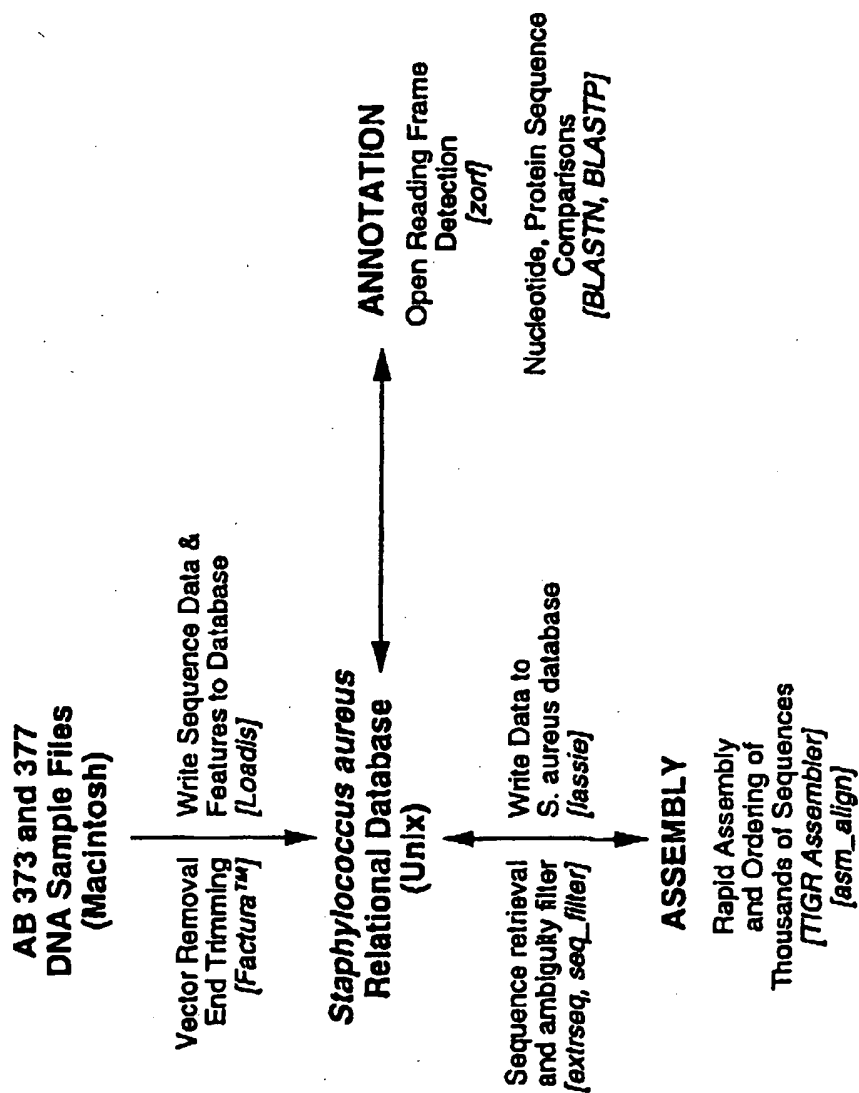
- (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTTAT TTCGTTCGnT 60  
 CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTTGGGGCC 120  
 CCGCCAACTT GCCATTGTCT GTAGAAATTG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180  
 CCCCAACTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240  
 AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300  
 TTGAAAAGAG CGTGTACAC GGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360  
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

Figure 2



(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10 AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG 60  
 TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGG AGAACCTAAA 120  
 AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT 180  
 15 GACCCTCTGA TAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC 240  
 TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA 300  
 TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT 360  
 20 TTACAGTCCG CCGCGTTTAG CACTTCGCTA CCCTCCAGCT 400

## (2) INFORMATION FOR SEQ ID NO: 3937:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC 60  
 35 CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA 120  
 TGTGTGCGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAGT 180  
 40 GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCTTC AGCGCCCCCA 240  
 TAATCGTTTA CATTAGCGGG TGTAAGTTAA TGGCAAAACC TCAGCCTTCC AAGCTGATGT 300  
 TGTGGGTTTC ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG 360  
 45 GTAGAGCTAT CGGCTGTAA CCGATCGGTC GTAGGTTCGA GTCCTACCTG TGGAGCCATG 420  
 GCTCyTTGGT CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC 480  
 CGTAGaGTYc ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA 540  
 50 TkGTTGgAGG aAGtTGtCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT 600  
 CACAAGCTT 609

## (2) INFORMATION FOR SEQ ID NO: 3938:

55

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10 TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGAATCGCT 60  
 AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTAACA CACCGCCCGT 120  
 CACACCACGA GAGTTTGTAAC CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180  
 15 CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240  
 CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300  
 GTGACATATT GTATTGAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360  
 20 GGGGTTAAG CGCACCTGA TAAACGTGAA GTCGGTGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3939:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTGATATG TCTGGTGAAT ATAGCAAGGA GGTCCACCTG 60  
 35 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC 120  
 CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180  
 TCGGCTGTTA ACCGATCGGT CGTAGGTTTC AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240  
 40 CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTCGAGTC CCGTAGAGTT 300  
 CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360  
 45 GGTTTCGAAC CCTTCATTTT CCACCATTTG GTTATTAAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3940:

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



ACACAACAGC TGTTCACAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60  
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120  
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180  
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240  
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300  
 10 AAAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360  
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

15 (2) INFORMATION FOR SEQ ID NO: 3941:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

25 ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60  
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120  
 30 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180  
 GGTCAATCAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240  
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300  
 35 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360  
 AAAAACTTCA GCAGGTTTTG CCAGTGGCnG TCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

50 CTCTGGATCA AAGCTTACTT ACAGTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60  
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120  
 CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

55

TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTnAT 300  
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360  
 5 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60  
 20 TTAAGCCCCT GTCGGTTTTC AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180  
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240  
 25 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300  
 CGCCTTATAT AGTTTGTAATA TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360  
 30 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 406 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60  
 45 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTT TGTAAACAAG 120  
 GCAACCCGTT GACCATTGCC CACACCATTT GATAGGAGCA TGTGCGCAAT GGCATCCACA 180  
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGACTAGCGC AACATGATTA 240  
 50 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300  
 GCATTCGATC GTTAACATGC GTATTGACCC AATTAGAAG TTCCTCCGTG CCGTTTGGTA 360  
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCnAAATAtC AATCAn 406

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTGCAAT 60  
 AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT 120  
 TTAAAGGAAA TTCAAGAAGA TGTTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT 180  
 GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT 240  
 CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGACCA 300  
 GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA 360  
 ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3946:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGThT TAATAGGnTC TGAAACGATA 60  
 CGTGTGCGG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT 120  
 GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC 180  
 CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCCGG 240  
 CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC 300  
 GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC 360  
 CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT 400

(2) INFORMATION FOR SEQ ID NO: 3947:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCCGGCCAGA GGA CT TGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60  
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180  
 10 GGCAACGTTT TACTCTAGCG GAANTAAATTC GNACTACCAT CGACGCTAAG GAGCTTAACT 240  
 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300  
 TAATTTATAC ATTCAAAAC AGATAGTAAG TAAAGTGAT TTTGCnTTTCG CAAAACATTT 360  
 15 A 361

## (2) INFORMATION FOR SEQ ID NO: 3948:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60  
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120  
 ATAAAGCGGA TTTCGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180  
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240  
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300  
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGCnGA ATAGGCCACC 360  
 GATACATCAC CAACAATTGG nA 382

## (2) INFORMATION FOR SEQ ID NO: 3949:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTTCTTTGT GTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60  
 GACCTTGCGG TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240  
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG 300  
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGn CTCAATGnGG 360  
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

## (2) INFORMATION FOR SEQ ID NO: 3950:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGGTTTT GCTTGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60  
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTAAACCAAA 120  
 AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180  
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240  
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300  
 30 TCCTAAAAGG nTAcnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360  
 GTGTACAAGA CCCGGGAACG nATTCACCG 389

## (2) INFORMATION FOR SEQ ID NO: 3951:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60  
 TTACCAATTT TAAATGAATT TAATAAGAC TTAGTGATA ACCTTGATAC CATATTCAAT 120  
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTC TATTACTCTG 180  
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240  
 GGTTCAACTG GAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300  
 AAACAnTGAT GGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

## (2) INFORMATION FOR SEQ ID NO: 3952:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCAT AAGTTGTTCT CAGTTCGGAT 60  
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120  
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCGTC ACACCACGAG AGTTTGTAAC 180  
 ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240  
 GGTGAAGTCG TAACAAGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300  
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360  
 GnTTTGGAAAT GTTnnTTAA CATTnCAAAA AAATGGGGCC 400

## (2) INFORMATION FOR SEQ ID NO: 3953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60  
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180  
 TTACTCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240  
 TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300  
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCTGGCAA 360  
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAATC GGTAATTAAT ATATGGATGA GTTTGCAATG 60  
 5 GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTTGA CCATAAAGCA 120  
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTT 180  
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240  
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTTGGAT TAGTGCTTTG CATCTTCATA 300  
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360  
 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

## (2) INFORMATION FOR SEQ ID NO: 3955:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTTC 60  
 GGTCCCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120  
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180  
 CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTCAAT CTACAAAAGG CACGCCATCA 240  
 CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCTT 300  
 35 TCCGGGGGTG CTTTTCACTT TTCnCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360  
 TAATTAGCTT AGGnGATGGT CCTCCAGAT TCGGAAGGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3956:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

ATAAAAATGG AGCAGAAGAC GGGATTGCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180  
TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240  
5 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300  
AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360  
10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3957:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60  
TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120  
25 AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCTACTA TTGATATATT 180  
CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240  
TTTTGGGGTG CATATTTTGT ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG 300  
30 ACCTGAGACA GGACTTACAC AGCCTGGCnA GACCATCCGT nTGTGGGTGA CTCTCACACA 360  
GCCACACATG GnGCCTTTT 379

## (2) INFORMATION FOR SEQ ID NO: 3958:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAATAA 60  
ATATATTCAA GGTCAgAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120  
45 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAAACAG CAGTAAGATA 180  
50 ATTTTCAATT AGAAAATATC TTAGTCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240  
GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300



AATAAGACAT TTGnCCAACT TGACACTACC ATTAAAACT

400

## (2) INFORMATION FOR SEQ ID NO: 3959:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

15

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60

CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT 120

20

TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180

CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240

GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300

25

CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360

CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3960:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

40

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60

TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120

GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180

45

ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240

ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300

50

CGCTGGAAC TCTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCA CGCCGTAGGC 360

TTAAGATTCC TGAAGTCTAG TGCCTCTGGC CAATTTCCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3961:

55

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

10

TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
GGTGATGGCG TGCCTTTTGT AGAATGAACC GCGGAGTTAC GATTTGATGC AAGGTTAAGC	240
AGTAAATGTG GAGCCGTAGC GAAAGCGAnG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

20

(2) INFORMATION FOR SEQ ID NO: 3962:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 361 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

35

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
ACGGGATTCG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
C	361

45

(2) INFORMATION FOR SEQ ID NO: 3963:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 375 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

EP 0 786 519 A2

AAGTGTCTTA TTTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120  
 GCGGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180  
 5 AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240  
 ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300  
 10 ATATTTACTA TCAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360  
 TTGGAATATA TTTAT 375

(2) INFORMATION FOR SEQ ID NO: 3964:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

25 AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACCTACA 60  
 ATTTTAAATA GATTTTTAAG ACCTTGTTGG TTTGTACAA TTAATGTGAC ATGACTAGGT 120  
 CTGACGTT TATATGCATC TTCATTACTG AGTTTTTGT TGATTCGTT ATGATTTAAT 180  
 30 ACGCCTAATT CTTTCATTG TTGAACCAT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240  
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300  
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAG TATCGATAAC 360  
 35 ACCATTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

(2) INFORMATION FOR SEQ ID NO: 3965:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT 60  
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAACCTAC CATTGCTTGT 120  
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180  
 55 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTGT TTCCAATTCA 240

TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360  
TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

(2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60  
TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120  
GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180  
AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240  
AAAGTATTTT AAAGTAAAT TACATGTTAA TACGTAtATA ATGGcGAGAC TCCTGAGGGA 300  
GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCtAGG AAAGCGAcnC ATTcAATACG 360  
AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

(2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60  
TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120  
AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180  
TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAACT GGTATCGGCG 240  
AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300  
GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360  
TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

10 ACCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTGCA ACCCGCGACC CCAACCTTGG 60  
 CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120  
 CACGCCGTAA nCTGAGGATC CTAAGTCTAG TCGTCTGCC AATTCGCCA CACCCGCAA 180  
 15 TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAGTCAG ATGCTCTACC 240  
 AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300  
 GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360  
 20 GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3969:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60  
 35 CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120  
 TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180  
 40 GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240  
 ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300  
 CATGTATTCC TATTTTAAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360  
 45 ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC 400

## (2) INFORMATION FOR SEQ ID NO: 3970:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 419 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GATAAGATCA GCCGAAAATG GATGGTGTGA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60  
 TTTTAAATGG CATTGTGTAC GACACCAITA CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120  
 5 CTATTTGGTG GTGTTGTGA TGCATCAAGT GCGTTTGC GA GTGCAGAGGC GCCACTGAKA 180  
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240  
 10 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300  
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360  
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTnCA ATGTCTAAT 419

## (2) INFORMATION FOR SEQ ID NO: 3971:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTATCTAA AAATCAGGCA TATAATTTCT 60  
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120  
 30 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180  
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240  
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300  
 35 CACCAACACT AAAAAATCCA TTAAGTGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360  
 GGGTTTCCAn AGTCCGTTAT G 381

## (2) INFORMATION FOR SEQ ID NO: 3972:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTcAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60  
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTGC 120  
 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300  
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360  
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3973:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCITTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60  
 20 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120  
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAT TGTGGCGATA TTTAAGGCAA 180  
 TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCTTGGA 240  
 25 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300  
 TTGTTTCTGC TTCATATTTT GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360  
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

## (2) INFORMATION FOR SEQ ID NO: 3974:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTTGTC ACGATAATAG 60  
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT 120  
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180  
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240  
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAAACT 300  
 TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360  
 CACTTGGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GGCGACCGCC CCAGTCAAAC TGCCCGCCTG	60
ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA	120
TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT	180
ACAAGCTGTG CCGAATTTCa ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC	240
TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTT ACCGAGTCTC TCGTTGAGAC	300
AGTGCCCCAA TCGTTAACGC CTTTCGTGCG GGTGGAACT TACCCGACAA GGanTTTCGC	360
TAACTTAGGA CC	372

(2) INFORMATION FOR SEQ ID NO: 3976:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT	60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC	120
CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA	240
ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT	300
TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TTAACTCATT GTCTGCTAAA	360
ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn	395

(2) INFORMATION FOR SEQ ID NO: 3977:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

5 TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60  
 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180  
 10 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGGCA CTATAAAAAT 240  
 GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300  
 TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360  
 15 CTTAAGTCTA AGTGCGTCTG GCCAATTTC GCCanACCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3978:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60  
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120  
 CTTTGGTTA CAGAAATTTT AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180  
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240  
 35 AGCTCTAAAA GTTGATTTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTGGGTG 300  
 GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360  
 GGATTCCGAA CCTCGGACCC TCnGAnT 387

## (2) INFORMATION FOR SEQ ID NO: 3979:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

50 TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60  
 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120

CGAACCTCTG GACCCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240  
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300  
 5 ACCAATTGAG CTAGGCCCGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360  
 ACCGCGGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

## (2) INFORMATION FOR SEQ ID NO: 3980:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTAGGTTTC TTGGTGGCT CTAGATTGT CCCTATTGTC ACAGCATTTG 60  
 CCGCAATCTT TTAGGTGTA TTGATGTTTT TCATTGGCC AAGCATACAA GCCGGCATT 120  
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGT TATGGCTTCA 180  
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG TTTTGGCAGA 240  
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACCTAGT TCAAGGTACG CAGAACATCT 300  
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360  
 30 nGTCAGCCGT TTTAATACGA GGATGTTCGG CTAnGTGGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3981:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60  
 45 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120  
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATT 180  
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240  
 GGATTTACA GTTGTCGCAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300  
 GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

## (2) INFORMATION FOR SEQ ID NO: 3982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 60  
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAAGCAA 120  
 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 180  
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240  
 TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300  
 AATATCGATA AATTGTGTTG ACGGTGCATC TGTAAGCTAGA GTTGGCGATA TTACATTGGA 360  
 AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

## (2) INFORMATION FOR SEQ ID NO: 3983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60  
 AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120  
 TCGAAAGAcG CGACAAGATT AATAACGCGT TAAATCTTT TTATAAAAGA AAACGTTTAG 180  
 CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT 240  
 AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AACATAGAT 300  
 TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360  
 GTTACTAACG ACGATATGCC TTGGGGGAGC 390

## (2) INFORMATION FOR SEQ ID NO: 3984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCCTGC CTTGTATCTG CAAATGTTTT 60  
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120  
 10 CGTTTCTTTT ATCCATTTC AATATTTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180  
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GGCCTTCTAA 240  
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300  
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360  
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

## (2) INFORMATION FOR SEQ ID NO: 3985:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60  
 ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120  
 AAAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTAT 180  
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240  
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAAC ATGThAATTT 300  
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360  
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

## (2) INFORMATION FOR SEQ ID NO: 3986:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCTTATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180  
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCCGT GCGGGAACGA 240  
 5 TTTTGTATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300  
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360  
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTGGAAC CCCCgcgagc CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60  
 CGGACTTGgg TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120  
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180  
 TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240  
 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG GGGACTAnCG 300  
 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCAG CTGGAGCTAA 360  
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60  
 ATGTTGCGCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120  
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG 180  
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240  
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGACTCCTAG GCGGTGAACG ACCATCCAAA 300

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

## (2) INFORMATION FOR SEQ ID NO: 3989:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15 CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA 60  
 ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA 120  
 GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG 180  
 20 CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC 240  
 ATCTGGAAAG ATGAATCAAA GAAGTAATA ATCTGTAGT CGAAAATGTT GTCTCTCTTG 300  
 AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCGTC GGAATCTGGG AGGACCATCT 360  
 25 CCT 363

## (2) INFORMATION FOR SEQ ID NO: 3990:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

40 TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG 60  
 GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTTACTT TTACTTTCTA GGATCGACCA 120  
 ATTCCCATTA AATTTTCTG TTGGCTTAAA GAAATTCAT CCAAATTTTC CCATATTTAT 180  
 45 ATCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAATGC 240  
 CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT 300  
 CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT 360  
 50 CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT 400

## (2) INFORMATION FOR SEQ ID NO: 3991:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTAA GAAATACAAT TTATTACCCA	60
GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAATTAAT CAAGTGAATT	120
TCTTTTGGTT ACAGAAATTT CAACAACTTT AAAGCANGTA TAATGATGAT TTTCAGCTTG	180
TACAAAGGAG AAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT	300
GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
ATTCGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

20

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

AGTGATGGT TATCAAAGAT TTGATACGAC GGTCAATTATT ATTACCGTTA TTGTATTAGT	60
CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTTGACA	120
TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
AGTTATCGTA GCACTTGAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC	400

40

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

55

TTATCAGAAG AACAAATCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120  
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GgncATTAC CCGTTGGATT ATTACCGAAT 180  
 5 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC 240  
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300  
 10 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT 360  
 CCGCCGGCAT TGAGAGCCTT AGA 383

## (2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTACCCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60  
 25 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120  
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnAAAC CnACTCCTCT TAACCTTCCA 180  
 30 GCACCGGGCA GGCCTCAGCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240  
 GATAAACAGT CGCTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTAAACC CTGAAAGAGC 300  
 ACCCCTTCTC CCGAATTACG GGGTCATTG CCGATTCTT AACGAGATTC GCTCGCTCAC 360  
 35 CTTAGA 366

## (2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60  
 50 TTCATTAAAA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTACTGGGAA ACGATTACAA 120  
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180  
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATT TGTGCTGAGC 240



GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG

359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA	120
TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTCTT AATTGAAATC ATCTTATGAC	180
TGCTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTnA GACATAAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTnTGCTG GGCAACGTTT TACTCTAGGC	360
GGAAnGTAAG TGGGACTTAC CATCGACGn TAAGGGGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCGGG CAGTTTGACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGGTTGGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAACATTA TTCCTGAAG 60  
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120  
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180  
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG AATTAAATTA TTTTAACAT CCATTACTTT 240  
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTTC ATGCTTACC 300  
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCAACAA GGTTAGGGCA 360  
 15 TAACACTTTC TATTTCCGAG GTAGCAAAGA CAAATTGCGA 400

## (2) INFORMATION FOR SEQ ID NO: 3999:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCCTTAG TGCTGCACtA ACGCATTAAAG CACTCCG<sub>8</sub>CT GGGGAGTACG ACCGCAAGTg 60  
 30 AAACtCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120  
 AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180  
 CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT 240  
 35 GGGTTAAGTC CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTa AGTTGGGCAC 300  
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC 360  
 40 CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

## (2) INFORMATION FOR SEQ ID NO: 4000:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

50 TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAA GGTTAGTTTG 60

55

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180  
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240  
5 ATTTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAAC TG ACAATGsCAA aGtTTATGAT 300  
GATTACmaAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360  
TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60  
CTTAACTTCT TGTTTTTCCG ATGACAGCTT CTATTAGAG AATGTCATGA TTATTTTATA 120  
25 TTCAC TTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180  
AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240  
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTCAATAA GTGTTTTCTC AATTTAAAAT 300  
30 CAAGTTCTTT CAAGGAAATC TGTTCTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360  
TTGTACCGTA TnATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60  
GACGTTTAAA CGTTTAAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120  
TTATGCATAC AGATCCAATG AAATCTTAC CTGAAGATGG TAGCTTGCAAG TTAAGTGCTG 180  
50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240  
CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

## (2) INFORMATION FOR SEQ ID NO: 4003:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTCCGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG 60  
 ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA 120  
 CGACAGGTGA TGGGGTTGAA AGTGTAAACn GCTACACTGG TCATGATGCT GCTAAACTAC 180  
 GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG 240  
 TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT 300  
 GGTTCCTCGG GTACCATTCC CGGTGCAC TTAAATTAG GAAAAACAC ATGATTTAAC 360  
 AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT 400

## (2) INFORMATION FOR SEQ ID NO: 4004:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC 60  
 GTGCCITTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT 120  
 GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC 180  
 AGGTGATCTA CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA 240  
 CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG 300  
 AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA 360  
 nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG 400

## (2) INFORMATION FOR SEQ ID NO: 4005:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

	ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
10	GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
	ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTA	180
	TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
15	GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
	ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA	360
20	TGTTGCCTAA TTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 444 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

	CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
35	ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
	GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
	AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGTGCTCTTT	240
40	AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
	AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
	TAAngAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
45	CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

50	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

TTTGAAGTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60  
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120  
 5 TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAAT 180  
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240  
 10 CGTGCCGAAC TGGAACTTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTCTT 300  
 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360  
 GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60  
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120  
 30 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTGGGTG 180  
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240  
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300  
 35 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360  
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60  
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120  
 55 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300  
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360  
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

## (2) INFORMATION FOR SEQ ID NO: 4010:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTAATAAATG GTATTTATTC ATCGAGTTAC 60  
 20 ATCTATAGTT TATTAAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120  
 TGATGACATT TAAAATGGCA GCGCTCTTTT ATTAAATTTT TGAAAATAAA AGGTTGTTGA 180  
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240  
 25 TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300  
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360  
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

## (2) INFORMATION FOR SEQ ID NO: 4011:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60  
 CGCTTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGACTGG CACTGCTCCC TCAGGAGTCT 120  
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180  
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTGA GAATTCCTCA AAATGATATT 240  
 50 TCGCGACATG TTAATGAAAT TGTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300  
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360  
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

## (2) INFORMATION FOR SEQ ID NO: 4012:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

TTTCACCTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA 60  
 AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTT TACTCTAGCG GAAGTAATTG 120  
 GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTGTGACAA TCGCTTGCTT CTTTCCTCTC 180  
 CTTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 240  
 TCAGATTCAA ACGTTTTTCA TCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG 300  
 ACGTTTTAGG CATAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT 360  
 TTTTGGCCTG GGCAACGTTT TnATnCCAGC GGAAnTnAAT 400

## (2) INFORMATION FOR SEQ ID NO: 4013:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCGCCCGC GTTTACCACT TCGCTACCCC 60  
 TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC 120  
 GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT 180  
 CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA 240  
 AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG 300  
 CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG 360  
 AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 4014:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

	ATTAGGACCT CAAGACGATA TTACTAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
10	AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
	CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTCT	180
	ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
15	CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTCT AAACGTTTTCT	300
	ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA	360
20	nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

	GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
	ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
35	ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT	180
	AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
40	GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCTGAAC	300
	TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG	360
	CCAGnTTATT CATATGA	377

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(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

ATGACGCACC TGACATCCTC TCGGTTTATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120  
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180  
 5 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240  
 CTCTGTACAT TTTTCCCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATGTA 300  
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTATAT CTCCTACGG 360  
 GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA 400

## (2) INFORMATION FOR SEQ ID NO: 4017:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAACG CCCGnCTGAC 60  
 25 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120  
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180  
 30 AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT 240  
 CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTCAAC GAGTCTCTCG TTGAGACAGT 300  
 GCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAACCTAC CCGACAAGGA ATTCGTTAC 360  
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4018:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAG ATCGAGCGGC 60  
 50 ATATGAGGCA CGCCAAGCGA TTCAAACAT TAATGAAAAC AGTCCGCCAA TATTAATTGT 120  
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180  
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360  
TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60  
TTGGGCTGTT CGCCATTAA AGCGGTACCA AGCTGGGTTT AGAACGTCGT GAGACAGTTC 120  
GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCCTTAGT ACGAGAGGAC 180  
CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240  
TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300  
ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360  
GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60  
AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120  
GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180  
ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240  
TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300  
TTTGTTAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360  
TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTACGGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

- (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG 60  
 CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG 120  
 TTTGCAAGTn TAAAGATCG TCCATTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA 180  
 GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTCCTTT AATGGTTGCA 240  
 GCAGTTAAAA AGACACATAT GATTTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT 300  
 TTGACAGTAC CTATAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTTATCAnT 360  
 AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT 396

## (2) INFORMATION FOR SEQ ID NO: 4022:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTGTA 60  
 TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAAG CATATATCAT 120  
 AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT 180  
 ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTTAG 240  
 CAGTAGTTGA CTGTAAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC 300  
 CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA 360  
 ACACAGAGGC TGGCGG 376

## (2) INFORMATION FOR SEQ ID NO: 4023:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60  
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcHGGCCAG AGGACTTGAA CCCCCAACCT 120  
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180  
 GGTGGAGAGT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240  
 10 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC TACTCTAGCG GAAnTAATTC 300  
 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA 360  
 CTCCTTGCTA TATCACCAGA C 381

## (2) INFORMATION FOR SEQ ID NO: 4024:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60  
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120  
 TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180  
 30 GGGTCTTGTA CACACGCCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240  
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300  
 35 AACAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360  
 ATTTCCGnAA CATCnTTCTT CCAGAAGATG CCGGTAATAA 400

## (2) INFORMATION FOR SEQ ID NO: 4025:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60  
 50 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120  
 CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCTGTGA CCACCTATAA TCGTTTTAAT 180

GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300  
 GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

(2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60  
 CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120  
 TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180  
 TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240  
 AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300  
 AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGtGnG 360  
 TGTTCCTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCATGTTTCG CTTGGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60  
 ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTAGTT 120  
 TCTGCTTCGG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180  
 ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTTAGA CGTTACTAAT TGGCTATTAT 240  
 CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300  
 AGTTAGTGCG TGCAGAAACT TGTTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360  
 GCCTCCGTTT TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60  
 CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120  
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180  
 15 TTCAAACGTT TTTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT 240  
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300  
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360  
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 4029:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60  
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120  
 TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180  
 TACTCTAGCG GAANTAAITC GGACTIONCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240  
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA 300  
 CATTCAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAACC ATTTGATTTT 360  
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

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## (2) INFORMATION FOR SEQ ID NO: 4030:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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5 GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60  
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTTGTTTCT 120  
 10 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180  
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240  
 TTTGAACGCC ATATAAATAA TGATTTTGGA TGATTCCTTT CAAATCAGGA TCTTCTATTG 300  
 15 CAAATTGTGG TTTGTnTTGG ATTTCACnTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360  
 TGAATCTATA CCCTGCATCT TGTAGCnTCC 390

15 (2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

25 TGGTTCGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60  
 CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120  
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTCCGCT 180  
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240  
 GAGGTATAGG TGTAATCCT ATCTCCGCT CCATAATTTA ATATTGCGG GGAGTAGTTC 300  
 35 CAACTTTTAG AACACGTTCC TTCCCGGAA GGAGGTATAn GTGTATCCTA TCTCCGCnC 360  
 CATAATGCCT TCCAAAGGGG AATTTTTTGG TTnACCATT 400

40 (2) INFORMATION FOR SEQ ID NO: 4032:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

50 GTATCGATGA GTTCTTTCGG TCGCTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60  
 ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120  
 55 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCCATG 180



TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300  
 AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360  
 5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT 400

## (2) INFORMATION FOR SEQ ID NO: 4033:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTT TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCCTTgGG 60  
 20 ACCGACTACA GCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACT CCCCCTCGAT 120  
 GTGAACCTCT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT 180  
 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240  
 25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATCTGT 300  
 AGGGAACCTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCAGTC AACTGGCCG 360  
 30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

## (2) INFORMATION FOR SEQ ID NO: 4034:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAAGTG nCGAAGCGAC 60  
 45 TTTCTGGTCT GTAACGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120  
 CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTAG GGGGTTTCCG CCCCTTAGTG 180  
 CTGCAGCTAA CGCATTAAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA 240  
 50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG 300  
 AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360  
 CAAATGACAG TGGTGCAngT TGTCTCACT CGTGTCGTGA 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

10 TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60  
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120  
 15 ATGTCAC TTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180  
 CATTAATACT ACGTATTAAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240  
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300  
 20 CCTGTTTTTG GATTTATGAA GGCTATTTGG GGTTCAC TCG AATGTCAGTT CGAGGAATAA 360  
 TAAAGTAAAC GAGAGCCAGG TTGTAATTA TGGCACTAAT 400

## (2) INFORMATION FOR SEQ ID NO: 4036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

35 TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60  
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120  
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180  
 40 CATTCTTCTA TCGATTTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240  
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300  
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC 360  
 45 TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4037:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60  
 5 TCTCGCTTAC TCATTTAGCT CTAATAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT 120  
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180  
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTTGCCT 240  
 10 GGCAACGTTT TACTCTAGCG GAANTAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300  
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360  
 15 TACnAACTC GTTGCCTCT T 381

## (2) INFORMATION FOR SEQ ID NO: 4038:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60  
 TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTAC TGTCATCGTA AAATGCAGCT 120  
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180  
 AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT 240  
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTGTGCTTA 300  
 ATGAATGCTT TnCTTCTTG GTGTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

## (2) INFORMATION FOR SEQ ID NO: 4039:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60  
 50 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120  
 CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCGGCAC TATAAAAATG 180

EP 0 786 519 A2

GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300  
CTAAGTCTAG TCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC 360  
5 GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTCTCTCTCC TTCGGCTCTC GCTTACTCAT 60  
20 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120  
TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAG 180  
AGACCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240  
25 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300  
GGCTCTCGCh TACTCATTTA GCTChACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360  
AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60  
GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAAC 120  
45 GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180  
TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240  
CTATCGATTG ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300  
50 CTGTATCACC ATCCATCATA CGATTCAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360  
TATTGGCACC CnAACCTTTG GACTTChAAT CTAACGGCCA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

10	GACTTGCAAA CGTTGTGATG ACGGTCAAGA AAAGTGGTAA CACACCAGAC GGACGTAAAG	60
	CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT	120
15	TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA	180
	ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT	240
	TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT	300
20	TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA	360
	ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA	400

(2) INFORMATION FOR SEQ ID NO: 4043:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

35	CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA	60
	AAGCAGGTCT TACAAACCAA GAAATTAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA	120
	AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT	180
40	TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAATCTT	240
	CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG	300
45	TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA	360
	TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAG	400

(2) INFORMATION FOR SEQ ID NO: 4044:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TGCGCTACTG G<sub>n</sub>ATAATAGC GAGGCTACCA 60  
 TGTGTGTTCA TCGTAG<sub>n</sub>CGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120  
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180  
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240  
 TCTTTTGTTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300  
 ATGCCATTAG GTAAGTGGAT TGATTGTAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360  
 15 CnTTTCCATT GCAAT 375

## (2) INFORMATION FOR SEQ ID NO: 4045:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60  
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120  
 CATTTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAATGAT TAATTGCACA 180  
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240  
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGT<sub>n</sub>G 300  
 ATTCAACTCC TCTGTATTAG AAATTGACC ATCAACAATT GTTATACGCT TTTG<sub>n</sub>AAGT 360  
 GGTGCGATAC TTTGGGGCAT CGCTGTGGGG TAGGGGG<sub>n</sub>Cn 400

## (2) INFORMATION FOR SEQ ID NO: 4046:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60  
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240  
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300  
 5 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACThACn GGATTCTGAG 360  
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

20 ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60  
 TTACGTTTCTAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTTACT 120  
 25 GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180  
 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TCGGACATTA 240  
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300  
 30 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTGT GATGACGGTG 360  
 GAATTTGACG GnGGACCAAG ATGChTGTTC CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

45 CAAACCATCT GACATAATAT AACTTGGAT GTTAGATAAG GGTtTGCCAA TTGGAATCGT 60  
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGAATCAGAT 120  
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTAAAC AAAGGATGCC 180  
 50 GTACTAGTTG CCCCGCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240  
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAACTGT 300  
 55 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

## (2) INFORMATION FOR SEQ ID NO: 4049:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60  
 GACACTACCT TCCCCTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120  
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC CAACATTTGA 180  
 ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240  
 GCTATATGAT TAnTATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300  
 ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360  
 CCCATACCGG GGTTCATCGTC CAATACACGT TCCAAncTnC 400

## (2) INFORMATION FOR SEQ ID NO: 4050:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCTATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTGG 60  
 GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120  
 GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTGATT GGAATTTCTC 180  
 CGCTACCCTC AGTTCATCCG CTCACTTTTC AACGTAAGTC GGTTCGGTCC TCCATTCAGT 240  
 GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300  
 CTAAACGCCT ATTCACTCG nTTTCGTACGG CTCCACATTT ACTGCTAAnc TTGCATCAAT 360  
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

## (2) INFORMATION FOR SEQ ID NO: 4051:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60  
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120  
 10 CCATTCGTTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCTAATC 180  
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240  
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300  
 15 CCAACATGTG GgntCCGGTT CATtGTGGTA ACGTGTtGGT AAAGAACGCA AGTGTATCGT 360  
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

## (2) INFORMATION FOR SEQ ID NO: 4052:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60  
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120  
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180  
 35 TTCCCCATTC GGAAATCTCT GGATCAAAGC TTACTIONAG CTCCCCAAAG CATATCGTCG 240  
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300  
 TTAATCnATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360  
 40 TTCATTAATT TTAAATGGCn CAATTTAACA 390

## (2) INFORMATION FOR SEQ ID NO: 4053:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180  
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240  
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300  
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTTCAGTG 360  
 CGATGATCGT GAAATTGANA CGCAnGATTT CCGATATAGA 400  
 10

## (2) INFORMATION FOR SEQ ID NO: 4054:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60  
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120  
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTCCTACAG 180  
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240  
 TACCTGCAAA TGCATATCCG CAAAATATCG TTTACTAATAT TTGGGnCATA CTCATCATAC 300  
 30 CACCCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360  
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

## (2) INFORMATION FOR SEQ ID NO: 4055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAATTC AAGTCTTCCA TAATTGGTTT AACAACTACT TCTACTTGTT 60  
 CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120  
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180  
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTTAC 240  
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300  
 55

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

(2) INFORMATION FOR SEQ ID NO: 4056:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 481 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAAACC ATCTCCAATA TAAAAATAAA 60  
 TTAAATTAAA TTCTCAGGGA CTGTCATGAC GCCACCTGTA TTTGCGCTAG TTACTAGGGC 120  
 AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG 180  
 GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTG TTAATCAAT 240  
 AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA 300  
 AATATGaCCA ACTGcAATAC CTCTTGTGGc ACCGGtAAAA ACGCCCATCA GTkAATTAAAT 360  
 GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG 420  
 nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT 480  
 G 481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG 60  
 ACCTTTCTTG ACTTGTGACA ATCGCTTGCT TCTTCTCTCT CCTTCGGCTC TCGCTTACTC 120  
 ATTTAGCTCT ACTAAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA 180  
 CTTGCGCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTA GACATAAAAA 240  
 AAAGAGACCT TGCGGTCTCA ATCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT 300  
 ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTCTTG GACTGTGACA 360  
 ATCGGCTGcn TCTGTnCCT 379

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60  
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120  
 TTTAAAGGCT AAACCTACCA TGTTTTCAAT GGATTTCCTAA AATGAATCAT CTGGGATGAC 180  
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240  
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTATT AAATGTTGAT ACACCATTG 300  
 AATACCATT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360  
 GGCGCATTTG ATTAAATGAT ACGTGGATTT GGACCCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 4059:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACCTA AGTnGAnCTA CCATCGACGC 60  
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120  
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180  
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTCGTCA GCTCCACATG 240  
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300  
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360  
 ATCCCGT 367

## (2) INFORMATION FOR SEQ ID NO: 4060:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

5 TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTGAG ACACCGCATT 60  
 CAGATTGAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120  
 GATTGAGATA GCGATTGAGA TTCCGACAGT GACTGAGATT CCGACAGTGA CTCGAGTCA 180  
 10 GACAGTGATT CGGATTGAGC GAGTGATTGG GATTGAGATA GTGATTCCGA CTCCGACAGT 240  
 GACTCGGATT CAGATAGCGA CTCGAGTGG GATAGCGACT CGGATTGAGA TAGCGATTGG 300  
 GACTGAGATA GCGATTGAGA ATCAGACAGC GATTGAGATT CAGACAGCGA CTCGACAGT 360  
 15 GACTGAGATT CAGA 374

## (2) INFORMATION FOR SEQ ID NO: 4061:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60  
 30 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCAGGAT ATTCATCTAA 120  
 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180  
 TTAAATAGA TTTTAAGAC CTGTGTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240  
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtKGTtG ATTTGTTAT GATTTAATAC 300  
 GCCTAAWTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360  
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTAGCCA AGAAATTCAA 420  
 40 ACCATGTTTA CC 432

## (2) INFORMATION FOR SEQ ID NO: 4062:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

55 TATCTTCGTT CTCAATAGAA TGATTAAAC CTTGATTTC TTTATCTAAA TGACTACCAA 60

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTTCGT 180  
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240  
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGANTCA 300  
 ATTAACGCAT CAGTATTAGG GANTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360  
 nTTGGATTTG GAGCTAACCA CATCCA 386

10 (2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60  
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120  
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTAAGC TGAGGCCGAC ACGTAGGGCG 180  
 ATGGATAACA GGTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240  
 CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300  
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360  
 CGAGTTCGTT GGrTTTCACA ATGGCC 386

35 (2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 60  
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120  
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180  
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240  
 AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

## (2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

15	AATTCCTTCG CTAATTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA	60
	GCAGGTGTAT ATTTTGATTG TGCATCGTCG TATCCTTTTG ATTCTAATT ATGATCAAAA	120
	CGACGCACGC CATATTGACT TGCCATTAAG TCAAAAATTG TAGCAATACG GACTTTGTCA	180
20	CCATTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA	240
	CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT	300
	GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTAA AGTTCCACTT CTTACCTTCT	360
25	TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC	400

## (2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

40	ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA	60
	GGAACAATCG TTATTAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA	120
	CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA	180
45	ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA	240
	GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG	300
	nATATTCATT TGTGTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT	360
50	GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC	400

## (2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

	CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATT A TTATTAAATT	60
10	ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTTCATAAA	120
	GTTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
	TTTGCAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG	240
15	AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTATA	300
	ATAAGGGCGG CTGAAGGGGA TCGAACCTC GAATGTCCGA ACCACAATCC GATGTGTAA	360
	CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

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(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

	TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAAG TGCTGCCAGT TGAGCGCCCA	60
	TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT	120
35	TGAGGATAAG ATAACCATTA AGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA	180
	AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAATTA	240
	GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
40	ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT	360
	AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

45

(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

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AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120  
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180  
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240  
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300  
 10 GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCh 356

## (2) INFORMATION FOR SEQ ID NO: 4070:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60  
 GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTG TTAAGGGGCG TTTAAGTAAT 120  
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180  
 GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240  
 30 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300  
 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360  
 AATGGATTAC CCAAGGATGC CATTAnTTA AGCCnGCCAn 400

## (2) INFORMATION FOR SEQ ID NO: 4071:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTCG CTA CTACACAC 60  
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120  
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG 180  
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240  
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTTAACAT 300

T

361

## (2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

15	ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG	60
	CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG	120
	GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT	180
20	TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA	240
	CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT	300
	AAACTTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT	360
25	GCGGTTnCCG TtnCATCAGG AntCATCTAG GCAAGGGGTC	400

## (2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

	GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA	60
40	TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT	120
	GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT	180
	TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT	240
45	GTAAATGATA CTGAACCACT TGTGAACCGG AACAAAGCAAT GGTAGTTACC AnaATTCTTG	300
	AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA	360
50	CCGGTAAGGG GGnCATCCT GGACCAAATT TAAAAGTTGG	400

## (2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

	TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA	60
10	TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG	120
	TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC	180
	CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCCCCAT ATCGGCGGAG TTATGCATCG	240
15	TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAn CTGTATTTCT ACGGACTGAT	300
	AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTTCAGT	360
	CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG	400

20

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 380 base pairs
	(B) TYPE: nucleic acid
25	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

	GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG	60
	GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG	120
35	CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA	180
	GCCCCCTCA AGATGAGATT TCCCAACTTC GGTTATAAGA TCCCTCAAAG ATGATGAGGT	240
	TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGAGCT GACGAATACT AATCGATCGA	300
40	AGACTTAATC AAAATAAATG TTTTGCACA AATCCACTTT TACTTACTAT CTAGTTTGAA	360
	TGATAAATTA CATCCATATG	380

45

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 380 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
50	(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

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TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120  
 CTACTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180  
 5 TCCATCGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240  
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300  
 AnCGGCATTG TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360  
 10 AAGGTTCTTA CCATGGTCAA 380

## (2) INFORMATION FOR SEQ ID NO: 4077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAGATTT AAATCGAAGA AACCAGCAAC 60  
 25 AGATTCTCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGACCT GCAGCTGGTA 120  
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180  
 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240  
 30 CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300  
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360  
 35 ACGGGCTCTT 370

## (2) INFORMATION FOR SEQ ID NO: 4078:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60  
 50 TGACTTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120  
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180  
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

TAAGAGGGGC CAACCATTGT TAGAATAAC AACGGTTGGC TCTTTAantG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

15	TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
	TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAAGTTGAT TCTTCTGACG	120
	CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
20	TTTGACCAAA TGTTGGGATT TTACTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC	240
	AGAATGGACC AGGCGCTACA CAGTTCACCTC TAATTCCTTT TGGTCCTAAT TCTTCTGAAA	300
	AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATaG	360
25	GCCAGGGaNT AAAACCCTGG AChAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

	TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
40	AGTAAATTA AATAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA	120
	TATATAGATC AACTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
	GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTAAATAT	240
45	GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATT	300
	GGTGCCTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
50	AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAAAA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTTCGACT CCCAAGTTAA	180
	ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

(2) INFORMATION FOR SEQ ID NO: 4082:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTT GTTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTTCCT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAACATTTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
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TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180  
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240  
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300  
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360  
 TGTnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCCGG 400

10 (2) INFORMATION FOR SEQ ID NO: 4084:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60  
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120  
 25 GTTCTTTTGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180  
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT 240  
 TTCTTTTtag TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300  
 30 TAAATAAACA TTCAAACTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360  
 ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

(2) INFORMATION FOR SEQ ID NO: 4085:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

45 TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120  
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180  
 50 GAACCAGCTG GAGCTATAGG CCCATTAAAT TGGAATGAAC AAACATTCAA AACTGGAATA 240  
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTTGT TCCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

5 GTCATTTGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGAATTCCA TGTGTAGCGG 60  
 10 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAACTG 120  
 15 ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT 180  
 20 AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA 240  
 AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAACTC CAAAGGAATT GACGGGCGCA 300  
 CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA 360  
 25 C 361

(2) INFORMATION FOR SEQ ID NO: 4087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG 60  
 40 AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA 120  
 CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT 180  
 AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA 240  
 45 GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC 300  
 AGGATTCGAA CCTGCGACCC CTTTCCCAA CCAAGTGCTT TTACCAAGTT GGTACTTCCh 360  
 GTATAATTTA ACGGGCCCGA TAGGAGTTTC GAACCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA	60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTTAA	120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAACC ATATTTAGTA AATACAGATG	180
GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA	240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA	300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA	360
GTCTGTGAGT GAGGGGTGTA TGGGAAAGTG GTTAAAATAT	400

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(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
GTGACAATCA AACGCTACAA CTAATTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG	120
CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAGTGA ACAACAACAT	180
TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA	300
TGGATTTAAC ACATTATGAA CGAGATGGTA AACTGCTAG CTCATTGCTG TTGAATTATT	360
ncATAACGGT ATCA	374

45

(2) INFORMATION FOR SEQ ID NO: 4090:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

55

EP 0 786 519 A2

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120  
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCGGT TGTGACAGTA AGTGACGCGT 180  
 5 TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAT GAACAATGTG ACGTATACGA 240  
 CGCAAGACGA ACATGGTCAA GTTGTTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300  
 ACAGTGCACC AGTAACAGTG ACACCACANT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360  
 10 TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTTCAA 60  
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120  
 TGGGGTGTGG GCCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180  
 GGGTGTGGGC CCCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240  
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300  
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360  
 CGGGGGCCCC ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 4092:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTCTCA TAACACAAGG AATTTCACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60  
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120  
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180  
 CCTGTGCAC CAGCTACACT TGCAATGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360  
 CATTTGACCT TCATTGTTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60  
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120  
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180  
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAATGTT TGGTTACCAA ACAAAAATGA 240  
 CATCATCGAA AAAGCAAAAG AAACCTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300  
 AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60  
 TGTCTTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTAA AACTCTTTAT 120  
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180  
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAA GCAGGCGCTC 240  
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGAATCG 300  
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAAG 60  
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAATACTG AAGATAAATA AGATTAAAAG 120  
 AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA 180  
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240  
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300  
 TGGTTCTTTG TCATTAGCCA CAGCTATTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360  
 15 CTCCTTGAGA GGAAATACTn ATTT 384

## (2) INFORMATION FOR SEQ ID NO: 4096:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTACACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60  
 30 TTACGCCTTT CGTGCGGGTC GGAAC TTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120  
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCTAG CTTCGCAGAA AGAGCCGACT 180  
 CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAC 240  
 35 CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300  
 GTTAACCCTn AAAGAGCACC CTTTCTCCCG AAATnACGG GGTCATTTTG GCCGAGTTCC 360  
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

## (2) INFORMATION FOR SEQ ID NO: 4097:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

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TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180  
 AGCGATTCGG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCAGAT 240  
 5 AGCGATTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300  
 TCAGATTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTCGGAC 360  
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTCAG 400

10 (2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60  
 CTGGATTGTA TGTAATTTG TTTAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120  
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180  
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240  
 TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300  
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGnAAT 360  
 GGCCAGTTTG CCAAGCACTG GTTTGACCA n ATGGnGGCA n 400

35 (2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

45 ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60  
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG 120  
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AACAGGGCT CTACCTCCAA 180  
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTCGGAGA GAACCAGCTA TCTCCAGGTT 240  
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCCG 300

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## (2) INFORMATION FOR SEQ ID NO: 4100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT	TGCCAAACAG	CATGCTTAAT	TTCAATATCT	TCTTTGACTG	CTTCGATATA	60
TAAATCAGCA	TCATCATTTA	CCAAGTCATC	ATCAAAATTA	CCATATGTTA	AATGACTCGC	120
TAGATTTAAG	TGGAATAGTA	GCGGCCGTTT	CTTATCTGTA	ATTTTATCGT	AAGATTTTTT	180
CGCAATGAGA	TTTGGATCGT	TTTTGTCCAC	TACAATATCT	AATAGTTTTA	CTTTAAGTCC	240
AGCATTACACA	AAAAGTGCTG	CCAGTTGGAG	CGCCCATGTG	GCCTGCGCCA	AGAACGGnTA	300
CTTTATTAAT	TGGTCATAGT	GAnTCCnCCC	ATTTAGTTGA	GGGATAAGAT	AACCATT	357

## (2) INFORMATION FOR SEQ ID NO: 4101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACCTCAGGC	TGGGGACATA	AATCAATATT	CTATGCTCTA	CGAATTATAT	TGGCAGTAGT	60
TGACTGGnCG	AAAATGCGCT	TGTAACAAGC	TTTTTTCAAT	TCTAGTCAGG	GGCCCCAACA	120
CAGAGAATTT	CGAAAAGAAA	TTCTACAGGC	AATGCGAGTT	GGGGTGAGGG	CCCCAACACA	180
GAAGCTGACG	AAAAGTCAGC	TTACAATAAT	GTGCAAGTTG	GGGATGGGCC	CCAACAAAGA	240
GAAATTGGAT	TCCAATTTTC	TACAGACAAT	GCAAGTnGGG	GTGGGACGAC	GnGATAAATT	300
TTGCGAAAAT	ATCATTTCTG	TCCCACTCCC	ATCAAAAGAA	TGACAT		346

## (2) INFORMATION FOR SEQ ID NO: 4102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60  
 GCGATTCAAC ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120  
 5 CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180  
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240  
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300  
 10 ATGAAAATGT ACGTGAGGAA ATThTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360  
 CAT 363

15 (2) INFORMATION FOR SEQ ID NO: 4103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGTTcAGGTT TAGCTGTGTG 60  
 ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120  
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGga TCACCAAGTT GAGCAAAGAA 180  
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240  
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300  
 35 GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360  
 AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60  
 ATTTTTTTAA AGTATTTAAA AGTAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120  
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

55

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300  
 ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60  
 TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120  
 TCAAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180  
 GTATTTATTA AAGGTGGCGA CGGTTTGTGAT TTCGGACACG TGGAAAGATT TATTCAAAC 240  
 CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300  
 CGGTAACACT TCATAAACT GCGGTTTGTh ACCATTACCT AATnGTCAAG GGTACGGCGT 360  
 TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTh 60  
 TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120  
 TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180  
 TTGAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAATA TAAGTTACAA 240  
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTTCATGGGA GAGTTTGGAT 300  
 CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360  
 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCh 400

(2) INFORMATION FOR SEQ ID NO: 4107:



- (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60  
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120  
 TTGGTTTTAA ATGCATTTC A GAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180  
 15 GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240  
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300  
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

20

## (2) INFORMATION FOR SEQ ID NO: 4108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

30 ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60  
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120  
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180  
 AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTGGT 240  
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGantGGTCA AGTAGTAGAA 300  
 40 AATCCTACTA CTATGGAAGA CGATnaAGAC GAACTGTTG TGGGTTGGCA G 351

40

## (2) INFORMATION FOR SEQ ID NO: 4109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

55 CCTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

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CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180  
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240  
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300  
 TTGCCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCTG 360  
 CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCTG CATTTGCGAA AGACTGGCAA GGACCACCAC 60  
 GTTTGCAAAA CGGAACAAGT TGGTCTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120  
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180  
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240  
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300  
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTG GCCATANGAA 360  
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

(2) INFORMATION FOR SEQ ID NO: 4111:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAGAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60  
 GTTGCCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120  
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180  
 50 ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240  
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GGCGGTTTAA TTTCCAGTAT TAGTACTAAC

400

## (2) INFORMATION FOR SEQ ID NO: 4112:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

15

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGCT CACATACGGC	60
TTCTGTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA	120
ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT	180
GAGTGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT	240
TATCACTCG GntTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT	300
ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC	360
GG	362

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## (2) INFORMATION FOR SEQ ID NO: 4113:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

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CAGGTGGTTT TGCGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG	60
AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA	120
AAGCTGTAGG TGACATTGAA GATTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA	180
ATCATACGCC GATTGAAGAA AATGTCACTG TTTACCAAGA GATCGTATCC ATTTTATCA	240
ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG	300
CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC	360
TAC	363

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## (2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 394 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTGA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG	360
	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

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(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAAGTGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT	120
35	ACGATTCCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GACACTGTAT TTACAACAGA ATATTGGTT CGTACTGCCA GGGAAGCTGT	300
40	TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG	400

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(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

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TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120  
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180  
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240  
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300  
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360  
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

## (2) INFORMATION FOR SEQ ID NO: 4117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60  
 25 TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120  
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TCGCCCCGGG 180  
 30 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCCC 240  
 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300  
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGCCCC 360  
 35 CCACCACAGG GAATTTGAA AGAAATnCT 389

## (2) INFORMATION FOR SEQ ID NO: 4118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120  
 GACGCTAAGG AGCTTAACTT CTGTGTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA 180  
 55 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACATA GATAGTAAGT AAAAGTGATT 240

ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360  
TATnAACCGA A 371

(2) INFORMATION FOR SEQ ID NO: 4119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 341 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60  
TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120  
AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180  
TGAAGCTACA CTGCTATTTT CAGCCCATn AAGCACGCTT TGAGACGCTT CTTCATTCC 240  
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300  
ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60  
GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120  
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTGCGGG GTAACCTGCA TCTTCACAGG 180  
TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240  
GGGTCGGAAC TTACCCGACA AGGAATTTG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300  
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360  
CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCAAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT	60
CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATACATAAT	120
AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC	180
ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC	240
ATTTGGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTC CGCCACCAAA	300
CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA	360
GCGGTGGTAC TACCAAnGAC CAGTGGAAGG TnCCAATTAA	400

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(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT	60
AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA	180
TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA	240
CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
TT	362

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(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

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CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120  
TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTTCGAT TTAAGAGGCCA 180  
5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240  
GCGATTCCAA ACATTAATGA NAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG 300  
ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352  
10 (2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA AACTGAATG GAGGACCGAA 60  
CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120  
25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180  
TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTCAGACA 240  
AACTTCCGAA TGCCAATTAA TTTGAACTTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300  
30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360  
GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

35 (2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

45 GGCTTATTAA TCAAAAAATT TATAAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60  
ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA 120  
TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180  
50 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240  
GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

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TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

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(2) INFORMATION FOR SEQ ID NO: 4126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

15	AATCTATATT TTAATTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT	60
	CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAAACT	120
	GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180
20	GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA	240
	TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT	300
	TACAAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGThATTG	360
25	AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

40	CGAAATTTGT AGTAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
	GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
	CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	180
	GTGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	240
45	CTGGAAGTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
	CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA	360
50	TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

	GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAATTT GGAGATTATC TGTCGTCTTC	60
10	AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTCG	120
	AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
	AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
15	GGGTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
	TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
	AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

20

(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

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	AGAGGTCCGT TGCCTTACCG CTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
	ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
35	CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
	GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CAAAATAAT	240
	GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTC TTGAACCGCT	300
40	TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG	360
	TThAACAGCC GGAT	374

45

(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 431 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

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ATTAAATTTT AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120  
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180  
 5 TATATAGTAA TCCGCCTTTT GTGTGACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240  
 TGGTAGTTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300  
 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360  
 10 TGAATAAant TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTTCATCATG 420  
 TTGGCGGTTT T 431

15 (2) INFORMATION FOR SEQ ID NO: 4131:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

25 TTTAGTTGAA GCGCGTGTTG TCGCATTTGC TGTTTGTTGC GGTGCTTCTA CTTTAGTTGA 60  
 GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120  
 TGATGTGGTG CTTCCACTTT AGGnAAntGA GTGTTGTCGC GTTTGCTGCT TCGGTTGTGC 180  
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240  
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGATACAT TCATTGAATC 300  
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360  
 35 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCAGTG TATGTCTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60  
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120  
 TGATCATTAT CAGATTCATC TTTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180

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TCAGCATTAT TTTTATTGT ATTGCGGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300  
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360  
 5 ATGGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTGTACC 60  
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAAGTG 120  
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAC GATTAATAGT 180  
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240  
 25 TTTCTCTATT CTTGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300  
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360  
 TAnCGGGTAC CGTTCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTA CTACGTT 60  
 CTACAATTTT ATCTTTTTTC GTTTTGTCAT AACATCTAA CATGTCGATG GCTTTATCAA 120  
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180  
 CGnAATATCT TCATCATGTT GGTGTTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240  
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300  
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

10 CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60  
 CAGTCATTTA TTTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA 120  
 ATTTTCAGTAG TCAAATTCGC ATATTGTAA ATTAACGGAT TCACTAATCG ATCATATAGA 180  
 15 ATGACATCCG CTTACAGTAT TAAACGCTCA GCCTTTTTTCG TCAAATAATT CGGATTACCT 240  
 GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300  
 CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360  
 20 GATTAAACA ATTTTTGATC GTGGGGGGGC AAATACATAT 400

## (2) INFORMATION FOR SEQ ID NO: 4136:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTCG CACTGTATGG 60  
 35 TGGGTTCCGA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120  
 ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180  
 40 TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240  
 ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300  
 TTATChTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

## (2) INFORMATION FOR SEQ ID NO: 4137:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

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TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTTCTCA 120  
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180  
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTAACA CACCGCCCGT CACACCACGA 240  
 GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300  
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGGCTGGG 360  
 10 AT 362

## (2) INFORMATION FOR SEQ ID NO: 4138:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCCGAAAT CTCTGGATCA 60  
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180  
 AGTCAAACGC TCACATACGG CTTCGTTTTTC ATTATTTTAA ATGCTCATTT ACATAAGTAA 240  
 30 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300  
 TTAAACGCGT TATTAATCTT GTGAGTGTTC TTTCGAACAC CAGCGATTAn TTChTGAGGA 360  
 35 ATTCAAGCCT AnTTAAAACC CTTA 384

## (2) INFORMATION FOR SEQ ID NO: 4139:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTGATCAAG ACAAATATGA CATTATTTTC 60  
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120  
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180  
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC 360  
 TTAATAATAA ATTTATATC ACACCGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60  
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120  
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTGCCTAAT 180  
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTA CTGCGTC 240  
 CCCCCATCGA TTAATAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300  
 AAGCCTGTCTG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCGGAAGA GCCTTCCTCT 360  
 GGAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA 60  
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120  
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA 180  
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240  
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300  
 AAACGCGTTA TTAATCTTGT GAGTGTCTCT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360  
 TnCAAGCnTA TTTAAACTC TTAATCACnC GGTTTTGcT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTTC ACTTCGCCAA GCCATTTTTTC 60  
 TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120  
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180  
 15 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 240  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300  
 GCCAAGCCAT TTTCTTGCGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360  
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCh 400

## (2) INFORMATION FOR SEQ ID NO: 4143:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTGACATG ATCCGCTAAA TGGATATGTG 60  
 35 CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120  
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CCAAAAACGT GGCGCTGTAG 180  
 CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240  
 40 TTGGAATTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300  
 GGCCATTCCG CTTTGCTGCC TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360  
 45 GAGGAAATG 369

## (2) INFORMATION FOR SEQ ID NO: 4144:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60  
 ATGTTTTAGT TGCCTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120  
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TCGCTCGAC ATAGTGCCAC 180  
 ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC 240  
 AACTAATTTA AGCTGTGCTT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300  
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAAACAA 360  
 CGGGAGnGGC 370

## (2) INFORMATION FOR SEQ ID NO: 4145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGGT 60  
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCGGACG TTGCTGGAGG TCTTGAAACA 120  
 GTCGCTGAAC GCCAAGGCCA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180  
 30 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240  
 TTGCTTTGTA GTCAGACCAG AACAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300  
 35 ATCGCACTTC GGCAATTGTT CTAACGCCCT AATTThAATT AAnTAATGTT CAAAGTAGGA 360  
 TTGAAGCGGG 370

## (2) INFORMATION FOR SEQ ID NO: 4146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTTC TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60  
 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120  
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTTGATCA TACTAAATTT 180

GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTThTTTT ATCAGGAGGA 300  
 GGATGGCGGT ATCCAATTTA TTCCATTGG GAAATATATG GnGCCCCGTT TTGGGAACnC 360  
 5 ATTTTTTGA AAGCCAAGCT 380

## (2) INFORMATION FOR SEQ ID NO: 4147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60  
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA 120  
 CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180  
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCACCT 240  
 25 TCGACGGCTA GCTCCTAAAA GGTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300  
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTgn CTGGGTTTAC 360  
 nT 362

## (2) INFORMATION FOR SEQ ID NO: 4148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTTGAA AATGATGAAC GATTCAGTGG 60  
 TTACGGCAAG CTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120  
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCGTGG 180  
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240  
 50 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300  
 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360  
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGCnCTA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10 CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA 60  
 CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC 120  
 15 AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AAGCCAGGTG GTGGTCAGGT 180  
 TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGGTA TTGTAAGTGG 240  
 CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACTCTGAAG TAATCTGATT 300  
 20 GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA 360  
 AACCATCATC ATATTnCAT CTGGTTAGGA CTGAAATGGC 400

(2) INFORMATION FOR SEQ ID NO: 4150:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35 AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT 60  
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG 120  
 GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 180  
 40 ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG 240  
 TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG 300  
 GCGAGTTACG ATTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG 360  
 45 AATAGGCGTT A 371

(2) INFORMATION FOR SEQ ID NO: 4151:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60  
 5 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTAACTTT ATTTATTCCT CGAACTGACA 120  
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180  
 TTGACTATAG ATGTTTTTCG TTCTGGTTC AGAAAGCTTT TGATTAAATT GGACTTTAAA 240  
 10 GTATTCCTCA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTGGAATT TGGTTTCATG 300  
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360  
 15 TCGTTT 366

## (2) INFORMATION FOR SEQ ID NO: 4152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAATA 240  
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300  
 CTAGCGGGAC GTAAGTGGCT ACCATCGAGC CTAAGAACCT TTCCTGGACT TGGTGGACAA 360  
 TCGCnTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

## (2) INFORMATION FOR SEQ ID NO: 4153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60  
 ACGTGCGATT GGATTGCACG TCTAAGCACT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240  
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300  
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360  
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

## (2) INFORMATION FOR SEQ ID NO: 4154:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

20 TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60  
 nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120  
 CATACCTCCA TCTCACCAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGTTGT 180  
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240  
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300  
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360  
 30 CCATACATCG TCATCGTTTG CACCGTCAA TACTGGTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4155:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60  
 45 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120  
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTG AGAAGAACG TAAATTTAAT 180  
 50 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240  
 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300  
 AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

## (2) INFORMATION FOR SEQ ID NO: 4156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTAGTTGGGCAC TCTAAGTTGA 120  
 CTGCCGGTGA CAAACCGGG GAAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240  
 CAAATCCCAT AAAGTTGTTT TCAGTTCCGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300  
 GGGAAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGATTACGT TTCCCGGGGT 360  
 CCTTGTTACA CACCGCCCGT 380

## (2) INFORMATION FOR SEQ ID NO: 4157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACCTTA 60  
 TGGATGATGG ATTCTGCCAA GTTAAATATA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120  
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180  
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTT TAAAGGGCAA 240  
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TGCCTCAGGA 300  
 GTTTCAGTGG ACCAGCTGGG GTGGATTGTA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360  
 ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60  
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120  
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180  
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

## (2) INFORMATION FOR SEQ ID NO: 4159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

25 AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60  
 TCTCTTGtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120  
 30 AATGGAATyT CTTCTTTTTT TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTACG 180  
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240  
 GGAACCTTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCGTCTCG ATGACCTGGT 300  
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTCTTCT 360  
 TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCGT 420

## (2) INFORMATION FOR SEQ ID NO: 4160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

50 ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60  
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240  
 TACGCCTTTC GTGCGGTCG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300  
 5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

## (2) INFORMATION FOR SEQ ID NO: 4161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60  
 20 GGCCCGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120  
 TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180  
 CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240  
 25 AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA GAAAAGCCTC TAGATAGAAA 300  
 ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

## (2) INFORMATION FOR SEQ ID NO: 4162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTAT 60  
 40 TTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120  
 GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180  
 45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240  
 GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300  
 GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360  
 50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

## (2) INFORMATION FOR SEQ ID NO: 4163:



- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTT 60  
 AAAATAATAC CAATCTCATT TTTAAATTCT AAACCTGGTT TCGTATAATA CGCTCTTAAA 120  
 TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180  
 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACITTA 240  
 GTTGnAAGGC GGTGTTGTG CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG 300  
 CGGTGTTGTC GCGTTTGGTT TTGnATGCGG TGCTTCTATT TT 342

## (2) INFORMATION FOR SEQ ID NO: 4164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60  
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTGGTAA GGTTCTTCGC GTTGCTTCGA 120  
 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTTCAACCT 180  
 TGCGGTGCGT CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240  
 AACCCCTTAA ACACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300  
 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGGCCA 360  
 nGGGGGTnCC nCCAAAACCT TGGGGATTTA ACGGTAAAAA 400

## (2) INFORMATION FOR SEQ ID NO: 4165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120  
 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180  
 5 ACTGTCTCAC GCAAACGTAA GGCATTTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240  
 TATTACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300  
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360  
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60  
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120  
 TAATGTTTCA ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAGCAAA 180  
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTTC 240  
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300  
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CnGGTnGTC 360  
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60  
 50 AGATACACAC CTTTACCGAC TATTTAAAAT ACACTTCACC AATTCATTTT AATTTAATGG 120  
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180  
 ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTITTTTGTA CCAAATGnTT GGGGATTTTA CTTnTGGGT TGTCCACCAG AAATTTGT

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(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

15	TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
	TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTCT AAATATGCAT	120
	ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
20	GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT	240
	CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA	300
	TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAATTG AGAGCTTnTG GnTTAGCTGG	360
25	ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

	ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
40	TCGTTAAATA AACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA	120
	ATTCAGGTCT CTTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
	AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TTGTTTTTCC	240
45	GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACITCA ATGTTATCAA	300
	TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
50	GTGTACnTCC ACGGTTTTCA TTTAAAnAACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60  
TTCCTTGTCTG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGCGGC ACTGTCTCAA 120  
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA 180  
AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA 240  
TAGGTAAGGA GCCTTTTGAA ACGTGAGCGC TANTTTACGT GGnAGGCGCT GGGTGGGGAT 300  
ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCANT TATCGTGGTG GGGAGACCAT 360  
GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG 395

20

(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG 60  
GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA 120  
GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTGGCTT ATTACCGAGT GGCGGTGGCC 180  
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT 240  
CCATGACAAA AGTACTGACG AATATCGCAT TCGGAANGCT CTACAAATGC CTTTGAGGCA 300  
CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT 360  
CGAAGTGGCG C 371

40

(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 361 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

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GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120  
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180  
 5 CCGGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240  
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CChGAATGAA CCGGTACGTG 300  
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCCG GACTATAAAA 360  
 10 T 361

## (2) INFORMATION FOR SEQ ID NO: 4173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60  
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120  
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180  
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTAAAGAT TTAGAAGGTA AAGATTTATC 240  
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300  
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360  
 AGnAATCCCA CCGTTGTAnG 380

## (2) INFORMATION FOR SEQ ID NO: 4174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60  
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTCGAAGTC GTTGATTTCa CACTGCCGAG 120  
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG 180  
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

GCCCAAGCGC TGTATTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360  
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

15 AGCCATGGCT CAGCGAGGTA GGACTCGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60  
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120  
 20 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAAC TTCTG TGTTCGGCAT GGGAACAGGT 180  
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240  
 AGTAAGTAAA AGTGATTTTG CTTGCGAAAA CATTTATTTT GGATTAAGTC TTCGATCGAT 300  
 25 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60  
 GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTGGTA CTGTTTTGT GGTGGCGAT 120  
 40 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTGTGGCG TGTGTGTGA TGGAGGTGTT 180  
 GTCACTTTAG TTGAAGGCGG TGTGTGCGCA TTTGCTGTTT GTTGCGGTGC TTCTACTTTA 240  
 45 GTTGAGGGCG GTGTTGTCGC GTTTGGTTTT GATTGCGGTG CTCTATTTT AGTTGAGGGC 300  
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG NAATGAATCG CGATGGAATA TCTCTATCTG NAAACAGATT TCTTTTTGTC 60  
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA 120  
 CCTAATGCTT TTAACCTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180  
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTC ATATGTTTCA CGATGTTTTA 240  
 ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300  
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAATTATAA TCCGAGGTTT TAGTTCCTCG 360  
 15 AG 362

## (2) INFORMATION FOR SEQ ID NO: 4178:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG NTGGAAAGAC GGTCTTGCTG 60  
 30 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120  
 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGAAGA CACGGTCCAG 180  
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC 240  
 35 GCCGCGTGAG TGATGAAGGT CTTGCGATCG TAAACTCTG TTATTAGGGG AGGACATATG 300  
 TGTAAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTACTAGGGG 360  
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG NAAGGGTTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4179:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

50 GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

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GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180  
CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTTCTGTCG TCTAGTTGGA 240  
5 AGAGAACGGC GGTGGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300  
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360  
10 GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGTACTAA GATGTTTCAG TTCTCCGGGT 60  
GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120  
25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180  
TAGTAACGTC CTTCATCGGC TTCTAATGCC AANGCATCCA CCGTGCGCCC TTAATAACTT 240  
AATCTATGTT TCCACCATTT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300  
30 nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60  
TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA 120  
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180  
50 TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240  
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTTCGATC CCGCTAGTCT CCACCATTAT 300  
TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343  
55



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60  
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120  
 GTCGATCTGC TAATTTTGCA AGTGCTACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180  
 CTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240  
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATT C CTCTTCATA 300  
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTTCTTTTCA 360  
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

## (2) INFORMATION FOR SEQ ID NO: 4183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATT 60  
 ACACAGCTGC AGGTGGTTCA TGGATTTTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT 120  
 ATTCACCTCA TCGGGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180  
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGGCC CGACATGTTG nATGCTGGCT 240  
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300  
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360  
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

## (2) INFORMATION FOR SEQ ID NO: 4184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60  
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGCATAGGT AATGGTTTAG TCGCAACACC 120  
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT 180  
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240  
 10 CAGTATGTTA CAACTAAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300  
 CATTGTATTG ATGnTCCTTG GGTnCATTTG CTGCATACAT GA 342

## (2) INFORMATION FOR SEQ ID NO: 4185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

25 AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTACTTGAAT 60  
 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120  
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTTCAGC GGAACACATG AAACGTTAGC 180  
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA 240  
 CGTTATGAAG TACAAGTTGA TGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300  
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

## (2) INFORMATION FOR SEQ ID NO: 4186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

45 CCCAAGCGGA ATTCTAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60  
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTG CATGAACCCC AAGCGTTTGC CGCATGATGC 120  
 TGTATTATTA ATTTATGGAA TGTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180  
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360  
 GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

5 (2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60  
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120  
 20 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAAGG 180  
 TGAAGAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240  
 AGAGCCCGTT AATGGGTGAT GCGTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTTG 300  
 25 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60  
 40 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCAAGTAC CGTGAGGGAA AGGTGAAAAG 120  
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180  
 GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240  
 45 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300  
 TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

50 (2) INFORMATION FOR SEQ ID NO: 4189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60  
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTTCAACAAC 120  
 TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180  
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240  
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACTTCCCC 300  
 AAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCCTCT 358

## 15 (2) INFORMATION FOR SEQ ID NO: 4190:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60  
 AAnGTACCAC CAAGTGCCGT CTGCCAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120  
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180  
 ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240  
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300  
 35 AAACCTAAAT ACGGTGGTAA TACCATTGT GntATTTGTT GTGAAGTATT GCGGTCATAA 360  
 TA 362

## 40 (2) INFORMATION FOR SEQ ID NO: 4191:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

50 TGATCACCCA TGTTCTGGAC TCCCAATTGA AATTGAATTG GGCATTGGA GTTTGTCTGG 60  
 nATTCGGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

55

nATTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240  
 CATTCACTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300  
 5 ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA 360  
 AC 362

## (2) INFORMATION FOR SEQ ID NO: 4192:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60  
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT 120  
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180  
 25 TTGCCGTA CTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240  
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300  
 GTTGTCATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360  
 30 CCAATCGGAA ATTGTAGCAT CnTTAATTTC CTAAAAGGTG 400

## (2) INFORMATION FOR SEQ ID NO: 4193:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60  
 TGTGATTAAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120  
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180  
 50 CTGATGGTTG CTCACTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240  
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300  
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATnTCATA TAATCCGGnA 360

## (2) INFORMATION FOR SEQ ID NO: 4194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60  
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120  
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180  
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240  
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300  
 AGTTtACGAT TTGgAttgCA AGGTtAAGCA GTAAATGTGG GAGCCGTA 348

## (2) INFORMATION FOR SEQ ID NO: 4195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG GCAACGTTCT 60  
 ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCGG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAAATA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300  
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

## (2) INFORMATION FOR SEQ ID NO: 4196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60  
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120  
 5 GAAGCAGGTG CGACACGTAT TGGTGGGAGC GCnGTGTTCA AATTATGCAA GGTTTAGAAG 180  
 CAGATTCAGA TTACTAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240  
 10 ATCGTGTA TTTAATCGTA ATGGATTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300  
 ATTTTAAAG ATGGAGGTTT ACATACTTTT A 331

## (2) INFORMATION FOR SEQ ID NO: 4197:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTGCG GCATGGGTGC 60  
 25 AGCTGCTATA TTTGAATATG TCGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120  
 TGTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180  
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTTAA 240  
 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300  
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATAN TATTGCTAAT GCnAGTAACT 360  
 35 nATCTGATTG T 371

## (2) INFORMATION FOR SEQ ID NO: 4198:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGThATTC TACCGCTGAA CTACTTCTGC ATATGCGGGT 60  
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120  
 TCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180  
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

TAAGAATAAA TGGTGGAGAA TGACGGGTTG GnACCGTCGA CCCTGTGCTT GTTAAGGCAG 360  
 ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGGCCTT GTGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60  
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120  
 CCATCCTAGT ACGCCAATAC CATTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180  
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCACGAACA TGTACAACAC TTGCTAAATA 240  
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300  
 ATGCTTTCCG TTGGCCCAAT TTAaaaaact GGATAACGTT CATnGTTACG TTCCAATTCC 360  
 TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60  
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120  
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180  
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240  
 CACACCATGG TTCAATGChT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300  
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACOGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
GCGGTTGGAC	370

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(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGThGG AATGAGtCGG	60
gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
GGaTTAgTGC AATAACCATC GCAACTGnGC CanACCTTGT GTTGGCTCGC CGCCTGAATT	240
CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTGC GTCTAGTTGC	300
TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTC	360
AAAGCAGCGT GCAAAAGGTT	380

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(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

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GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTGTAGAT 120  
 CCAGGTCCAA CTGGTTTAGA AAAGAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT 180  
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240  
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG 300  
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360  
 10 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCITCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60  
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120  
 AGACAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180  
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240  
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300  
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

## (2) INFORMATION FOR SEQ ID NO: 4205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60  
 ATACCTCGTT CCGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCGCAA ATATTAAATT 120  
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCOA GGAAGGAATG TATTCTAAGA 180  
 GTTGAAATAC TCCCGCATT TATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240  
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

## (2) INFORMATION FOR SEQ ID NO: 4206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTA ATCCAGAAA CTTGAGGAT GTCATAATA GTGTGAATAT TACATTCCCA 60  
 AATCCAAATC AATATAAAGT AGAGTTTAAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120  
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180  
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240  
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300  
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360  
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

## (2) INFORMATION FOR SEQ ID NO: 4207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60  
 CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120  
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180  
 GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240  
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300  
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360  
 AATGTAACAC GCCGGTGA CTATCCAGCT GAATAGACGC GT 402

## (2) INFORMATION FOR SEQ ID NO: 4208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60  
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120  
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180  
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240  
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300  
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360  
 15 CAGCATCTGG TACnGGTAAG 380

## (2) INFORMATION FOR SEQ ID NO: 4209:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60  
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120  
 CATAATGAGT TAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180  
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240  
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300  
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360  
 ATTGGCCCCG TGCCAACnTT TATATTGAAC CAAGCACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4210:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCACAACC ACAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

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AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGACTTCA 180  
AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240  
5 TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTA CTGCGAA ATTATTGTnT GATTTGCCAG 300  
TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC 60  
GTTTTCACTT CGCCAAGCCA TCTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120  
AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180  
25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240  
TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300  
ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

(2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 334 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
45 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240  
TTTTAGCACA TAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300  
50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

- (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAAA TCGTTACGCC TTTCGTGCGG 60  
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120  
 TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180  
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240  
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300  
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

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## (2) INFORMATION FOR SEQ ID NO: 4214:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

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CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT 60  
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120  
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180  
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240  
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300  
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAAnTG TGGACAACGn 360  
 TGG 363

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## (2) INFORMATION FOR SEQ ID NO: 4215:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

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TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120  
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTGGAACCG ACACTCCACA 180  
 5 AGTGGAACGG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240  
 AAACAAAAAA CTTCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300  
 10 CTCGTTCGGG GAAGGACGTG TTCTAAAAGT TGACTACC 338

## (2) INFORMATION FOR SEQ ID NO: 4216:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60  
 ATGCTTAGAG TTAACCATG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120  
 25 TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180  
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTAA 240  
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTAA CCAGATCCAG AAAGTCTTT 300  
 30 AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360  
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

## (2) INFORMATION FOR SEQ ID NO: 4217:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

45 AGGGAATCGA ATTTTCTTTC TCTTCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60  
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120  
 50 CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240  
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA 300

## (2) INFORMATION FOR SEQ ID NO: 4218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA 60  
 AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTTCGATTG GAATTTCTCC GCTACCCCTCA 120  
 GTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT 180  
 TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC 240  
 TATTCAGACT CGCTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT 300  
 AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTAA 345

## (2) INFORMATION FOR SEQ ID NO: 4219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AAACGTTTTTC 60  
 ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA 120  
 AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTGCCTGGC AACGTTCTAC 180  
 TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240  
 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA 300  
 CATTCAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT 360  
 CTTTCGTC 367

## (2) INFORMATION FOR SEQ ID NO: 4220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

5 AAGAGCCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180  
 10 nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240  
 TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300  
 CGGCATGGGA ACAGGTGTGA CCCCnTGGC TATAGTCACC AG 342

## 15 (2) INFORMATION FOR SEQ ID NO: 4221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TGCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60  
 TGTGAActCT TGGGGGAGAT AAGCtGTTAT CCCCggGTA GCTTTTATCC gTTGAGCGAT 120  
 30 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180  
 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTAT GAATGATTTC CAACCATTCT 240  
 GAGGGAACCT TTTGAGCGCC TCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAActGC 300  
 35 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

## (2) INFORMATION FOR SEQ ID NO: 4222:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAActAGAT AAGTAAGTAA AATATAGATT 60  
 50 TTACCAAGCA AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA 120  
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180  
 GAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

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ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360  
 G 361

(2) INFORMATION FOR SEQ ID NO: 4223:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60  
 TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120  
 ATCACCGTAC CGGTTTCGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180  
 ATAGAGCGTT TGA CTACGGA TCAAGAGGTT ATGGGTTTCA CTCCTATCGG GCGCGCCATT 240  
 TTAAATTA TGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300  
 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360  
 GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60  
 GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120  
 TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180  
 TAGTGTCATT TCCAGCAATT TGTTCCGGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240  
 GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300  
 CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360  
 TTCGATCCAG TTGATAATT GAACCTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

- (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

10 GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60  
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTCACCA TTCAACCAAA ATTGATCCTG 120  
 TGTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180  
 15 TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTATnAG 240  
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300  
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

20

## (2) INFORMATION FOR SEQ ID NO: 4226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

30

TGACGGGTTT GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60  
 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAnGTAAG TTCGnACTAC 120  
 35 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240  
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300  
 40 TCCACATGTC ACCATGCTTC CACCT 325

## (2) INFORMATION FOR SEQ ID NO: 4227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

50 GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TnTTCAACA 60

55

AACCTTACGC AAGAAGCAGC TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180  
 AATTCAAGnA ACTGCTGAAG TTITAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240  
 5 AGAAGCTGGT GTTGGTAAAA CTGCCATTGT TGAAGGTTT AGCACAGGCA ATCGTTGGAA 300  
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

20 AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60  
 TCGAACCCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT 120  
 GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180  
 25 AACTATGCCC CTATTAAAAA TAATAAATGG AGGGGGGCAG ATTGGAAGTG CCGAACCCGA 240  
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300  
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

30 (2) INFORMATION FOR SEQ ID NO: 4229:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60  
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120  
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180  
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAAATTTAG AGGTGATGTT 240  
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300  
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC 360  
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTTC 60  
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCACCT ATCGGTCACCT AGAGAGTATT 120  
 TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTA CTCA 180  
 GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCATC 240  
 TTTcCAGATG ATTCGTCTAA TGTCGTCCTT TGTAAC TCCG TATAGAGTGT CCTAsAACCC 300  
 CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG 339

## (2) INFORMATION FOR SEQ ID NO: 4231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

GAAGTCATAT GCATACACTT GGTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG 60  
 AATTTGTTA CCTGCGCCTT CTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120  
 TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC 180  
 AAAC TTTTTC ACTTCAGACT GACGTCCGTh TTTAGTTAAT GGGTCAATAA TTCCATAACG 240  
 ATGAGTATCT GCTTCCGGAA CTTCITGGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA 300  
 AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

## (2) INFORMATION FOR SEQ ID NO: 4232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

EP 0 786 519 A2

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG 180  
 5 GAACCACCGG ATCACTAAGT CCGTCTTTG ACCCTGCTCG ACTTGTAAGT CTCGCAKTCA 240  
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTC AAC CATCTGAGG GAACTTTGaG 300  
 10 CGCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG AACTGTCTC 360  
 CCACCACGAT AAGGTCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60  
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120  
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180  
 AATATATGTT AAGTGAAAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240  
 30 AAGCAGCCGT CATTAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300  
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTtn 355

(2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCGCCTGTC 60  
 ACGCAGAGAT CGCGGGTTG ATTCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120  
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180  
 50 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240  
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300

TTAATAATTT TAATAAGGG CATAnTTCAA CGGTAnAATA

400

(2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA	60
GGCGTAATAT CACTCTTTGC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA	120
TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT	180
TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCTAAAC CACTATCTGA TACAAGACCA	240
ATTGCATGnT TTGTTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA	300
CCTTGTGAGG TTGATAGCG ATACCGTCAC CCATGCATTT T	341

(2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCCCTAAAT ATAATTTTAC	60
AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCGA CCTCACGGGT ATGAACCGTA	120
CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA	180
GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCAG CTGAGCTAAG	240
CCCCATAAT AATTACAGTA TATCGGAAG ACAGGATTG AACCTGCGAC CCCTTGGTCC	300
CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT	360
TGAACCCATG AACCTnTTGA TCnTAGTnC AAACGGTCTA	400

(2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5 nAnTTCTTGA CTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60  
 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120  
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180  
 10 ACGTTACCAG CAATAATTTT ATTTTGTGCT TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240  
 CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300  
 CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAATT 360  
 15 GTATTTTCAG GAAGTC 376

## (2) INFORMATION FOR SEQ ID NO: 4238:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60  
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120  
 30 TTTTCTGGGA AAAGTTTGCG CATTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180  
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240  
 GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTTCCTCCG TATTGAAGGC TACTTGACGA 300  
 35 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

## (2) INFORMATION FOR SEQ ID NO: 4239:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60  
 50 TTCGGACACG TAGAAAGATT TATTCAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

55



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TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240  
 AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT 300  
 5 GAACTACATT ACATTTGTCC AnTACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60  
 20 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120  
 TTATGAATGG CATACATGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180  
 CAAGTGCGCA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240  
 25 TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300  
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360  
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

30 (2) INFORMATION FOR SEQ ID NO: 4241:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60  
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120  
 45 CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180  
 TGTTGGGGCC CCGCCAACTT GCATTGTTTG TAGAATTTCT TTTCGAAATT CTTTATGTTG 240  
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300  
 50 GGACTTTTAT GGCGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

55

(A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10	TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA	60
	TCATCTAAAT GATTTTTAGC TGTGATTAAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC	120
	TCTTGACTT CTTCACTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG	180
15	CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA	240
	TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTTGAACC ATAATCTTTC	300
	ACAATTnCAC TTGTGTTGAC AGATGAGnGG CCGTGCACTA AGGACTGGAT ACACTACGAG	360
20	TGACCGGACT GCTTCGGGnA ATGTGATGA	389

## (2) INFORMATION FOR SEQ ID NO: 4243:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

35	ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT	60
	TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT	120
	GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT	180
40	GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTh TTTTGAAAT GATTGCGGCG	240
	ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTCCGAAT	300
	AAACGACAAG GTGCAATTTT GG	322

## 45 (2) INFORMATION FOR SEQ ID NO: 4244:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120  
 ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180  
 5 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240  
 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT 300  
 10 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

## (2) INFORMATION FOR SEQ ID NO: 4245:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTGTGAAGCA CACGGTTTCA GGTCTATTT CACTCCCCTT 60  
 CCGGGGTGCT TTTACCTTT CCCTACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120  
 25 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180  
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTG 240  
 30 ATCTTTCCAG ATGATTTCGTC TAATGTCGTC CTTTGTAAC CCGTATAGAG TGTCTACAA 300  
 CCCCAACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTTCG GCCGnAA 358

## (2) INFORMATION FOR SEQ ID NO: 4246:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TCGGTTAGA TCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60  
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 50 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300  
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338  
 55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

```

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA      60
AGTCGGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT      120
ACACTCTATG AATGATTTCC AACCATTCTG AGGGAACCTT GAGCGCCTCC GTTACCTTTT      180
AGGAGGCGAC CGCCCACTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG      240
GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC      300
TCACGTTTCA AAGnTCTACC TATCCTGTAC A                                     331
  
```

(2) INFORMATION FOR SEQ ID NO: 4248:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

```

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG      60
ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG      120
GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTTC TCATTCTTCA AATAAACCAG      180
AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG      240
GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA      300
ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC      360
TAATGCCCAA T                                     371
  
```

(2) INFORMATION FOR SEQ ID NO: 4249:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60  
 ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120  
 TGTGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180  
 TCGTTAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240  
 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300  
 GTTTCATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

## (2) INFORMATION FOR SEQ ID NO: 4250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

GAGCCCAAAC CAACAAGCTT GCTTGTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60  
 AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120  
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180  
 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240  
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300  
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCCTGCCTT TT 352

## (2) INFORMATION FOR SEQ ID NO: 4251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

CATTTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60  
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTCAC 120  
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180  
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTC ACGTGCTCCGT 240  
 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

## (2) INFORMATION FOR SEQ ID NO: 4252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60  
 AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120  
 CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180  
 ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT 240  
 ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300  
 TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCEAA CCTGTTAAAT 360  
 CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC 400

## (2) INFORMATION FOR SEQ ID NO: 4253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60  
 ACTAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120  
 GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180  
 TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT 240  
 GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300  
 AGnCAGCGAC TCAGACTTCA GACAGCG 327

## (2) INFORMATION FOR SEQ ID NO: 4254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTTAT 60  
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120  
 TAGGATTGTn CTnTTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180  
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240  
 GGTGACCTTC ATGCCAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300  
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

## 15 (2) INFORMATION FOR SEQ ID NO: 4255:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60  
 CTCTATAGTG TTGTATTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTC 120  
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTAAATACA 180  
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240  
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA TATAATTCAA AAAAGGGTCG 300  
 35 AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA 344

## (2) INFORMATION FOR SEQ ID NO: 4256:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTCAAT ATTAAATTGC 60  
 50 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120  
 AAGCTAAATT CTGCGACAAA GCCGCCCATT GCAGCACCGA CAGCCACACC AATATTTTGC 180  
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CGGCCATTG GCCCACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

## (2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

15	GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCCGACTAT TTTTGAAAAG AGCGTGTTAC	60
	ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT	120
	TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT	180
20	AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT	240
	TTCGGTTTTG AGACAATTCG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC	300
25	TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT	360
	GCGGAGTGA	369

## (2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

40	CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT	60
	TTTTTAAATA CTAAATACA TGTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC	120
	CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT	180
45	GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA	240
	ATGTACCAGT GTTGAATAAA GCRAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA	300
	CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT	335

## (2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA 60  
 GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120  
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180  
 10 CTGCGGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240  
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300  
 CTGTGTCGGT TTGCGGTACG GGCA 324

15 (2) INFORMATION FOR SEQ ID NO: 4260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG 60  
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120  
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 180  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240  
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAACGTTT AGCAGACAAT GAGTTAAAnTT 300  
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCAITGAA AATnATGAAA ACGAGCCCGT 360  
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

40 (2) INFORMATION FOR SEQ ID NO: 4261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60  
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

55

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240  
 TTGTCTTGTT TATATTATGT GATTCAAACA TTAGTAGTCT TGGTAAATCT AATTCGTAAA 300  
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60  
 20 ATTTTGACGT TTAGGCATA AAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120  
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCnTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 25 ACTCATtnAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCTAC GnaATGTCGG AACCACAATC 60  
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120  
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA AATAATAAAT 180  
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240  
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300  
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCAGACTC CTGAGGGAGC	60
AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTGCTGT	180
TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
TTTTTGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

20

(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT	60
GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
AGTAACGCAA TCATTTCTTC TAAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA	180
TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

40

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTAAAGTCCT GTGCGTCTGC	120

55

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240  
 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TGCGTCTGCC AATTCCGCCA 300  
 5 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

## (2) INFORMATION FOR SEQ ID NO: 4267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTTT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60  
 20 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCGTGAG 120  
 GTnTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATT 180  
 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240  
 25 ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300  
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

## (2) INFORMATION FOR SEQ ID NO: 4268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60  
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120  
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180  
 TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240  
 GAATCGTTCA TCATTTTCA nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300  
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360  
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

## (2) INFORMATION FOR SEQ ID NO: 4269:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAAGCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60  
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120  
 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180  
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240  
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCCA ACTTCGGTTA TAAGATCCCT 300  
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

20

## (2) INFORMATION FOR SEQ ID NO: 4270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30 AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTGTGCCATT 60  
 TTATTTTTTA ACCAAAATTT GATTAAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120  
 35 TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACCTCTGT GTTCGGCATG GGAACAGGTG 180  
 TGACCTCctT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240  
 40 GTAAGTAAAA GTGGATTTTG CTTGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300  
 GTATTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360  
 CGCAGGGGAnC 370

45

## (2) INFORMATION FOR SEQ ID NO: 4271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

55

ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTAA CACAATTATG ATTGGCGTAA 120  
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACCTG TGGCACAATG 180  
 5 GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtA ATGGGAATAA 240  
 AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300  
 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCCTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60  
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCCGATT ACTAAACCTT 120  
 25 TCAAACCTTAT CGATGATTTT ACCGTTATGA ACTTTCACAG CTGCAAnTCG ATGATTTTAT 180  
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240  
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC 300  
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGACTCTAGA CTCTTATGTT 60  
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120  
 TATAGAATGG TGTACATCCT GAACCATAAT CCTTAACCTG GAAAACATCA ACAGTCTTCT 180  
 50 TATTAATAGG ATTTGCAATA ATACCGCTT GCTTTTTCAA ATCATTCTTA AGTGTGTCGA 240  
 TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300  
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA 60  
 GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA 120  
 GTTGCTTCTG GCGGTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA 180  
 ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA 240  
 TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG 300  
 CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG 360  
 GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCCGGTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC 60  
 TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT 120  
 TAATTCCTAT TAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA 180  
 TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG 240  
 GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT 300  
 TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n 341

## (2) INFORMATION FOR SEQ ID NO: 4276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

EP 0 786 519 A2

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCTT 60  
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTC TTTATTTTAA ACATGAACAA 120  
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180  
 TTAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240  
 CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300  
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360  
 ACGGTCCG 368

15 (2) INFORMATION FOR SEQ ID NO: 4277:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTA CTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60  
 GAGGGACCAA ACATTGGATT GATTA ACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120  
 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180  
 30 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAATCTAAA 240  
 TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300  
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTACT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60  
 CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120  
 50 TGCTTTGTGA ATCGGATTCTG CTCGTGCTTG TACTTGTGTA GTTTGAGGCA CTTTGGCTTG 180  
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

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TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTCAC TTGAATGATG TTGAGTCGGA 360  
 TTCACCTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4279:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATTAGACA TAAATCTAA AAmCAGCAGT AAGATGATTT 60  
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120  
 20 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAATA TCAATTTTAC 180  
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240  
 AGTTAGCTAC CATCCTCGCT AAGAACCCTT CTTGACTTGT GACAATCGCT TGCTTCTTTC 300  
 25 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
 40 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120  
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180  
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240  
 45 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300  
 CCTATAATCG TTTAATCGAT GGGGGG 326

50 (2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG 60  
 GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120  
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180  
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240  
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGAAT ATATCCTTAG AAAGGnAGGT 300  
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CTTGTTGAC GACTGTCACC CCAAGCATTT 360  
 GTGCCCAAnCn 370

## (2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

30 GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60  
 CTTACAGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120  
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180  
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240  
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300  
 GAAACATTAG GnATATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360  
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn 400

## (2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

55 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

TCTGTCCCAC TCCCGATTAT CTCGTGCGAA TATTTTTTTC AAAGCGATTT AAATCATTAT 180  
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTGGA TTTGGTGAAA 240  
 5 TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300  
 CTnAATCCAT GATAGACTGn CCCG 324

## (2) INFORMATION FOR SEQ ID NO: 4284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAAC TTCTATTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60  
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120  
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC 180  
 25 AAGATGCGTT ATAAGCATTG GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240  
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300  
 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTAAAGCCA GATTTACGTG 360  
 30 ATGTCTAACA AGTTTTnTnC GCTAAAATCn GGGTGGAGAC 400

## (2) INFORMATION FOR SEQ ID NO: 4285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTCTT TGTGTTTACT TTTATTTTG ACGTTTTAGA CATAAAAAA GAGACTCAGC 60  
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120  
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180  
 TACTCATT TA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240  
 50 TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300  
 AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480  
 ACTCGTTGCG CTCTTTTCTC GTTTCGTGAG ATTCAAACGT TTTCACCTCG CCAAGCCATT 540  
 5 TTTCTTTGTG TTTACTTTTT 560

## (2) INFORMATION FOR SEQ ID NO: 4286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GtATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60  
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAGA CCGTCTTGCT GTCACCTATA 120  
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180  
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240  
 25 GGAGGCAGCA GTAGGGAATC TTCCGCAATG GCGGAACTG GACGGAGCAA CGCCGCGTGA 300  
 TGnATGGAAG GTCTTCGGAT CGTAAAACTC TGTTATT 337

## (2) INFORMATION FOR SEQ ID NO: 4287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60  
 CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTAA TTCATCTAAT TCCTTACCCT 120  
 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180  
 45 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240  
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300  
 50 GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

## (2) INFORMATION FOR SEQ ID NO: 4288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCAC TG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC 60  
10 GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTCGC TCACCTTAGA ATTCTCATCT 120  
TGACTACCTG TGTCGGTTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTTCTCGG 180  
CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA 240  
15 CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC 300  
GGTTTnGCCT ATCCTA 316

20

(2) INFORMATION FOR SEQ ID NO: 4289:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

30 TTnTTTATGT CTAAAACGTC AAAATAAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT 60  
GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAGTAT AATAAAAAGC AGTCATAAGA 120  
TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTCTTAC TATGTGTTAA ATTAACAATG 180  
35 AATATAACAT CTTATTTTCA TTAATATAAA TATTGGAAGG ATCGAnATGA TTTACACGTT 240  
GTTTGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG 300  
TATTTTGAGA GATTTTTTAA GT 322

40

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

50 TCATTTAGCT CTACTAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT 60  
CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT AGGCATAAAA 120

55

EP 0 786 519 A2

CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240  
GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACTCGTTG 300  
5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60  
20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT 120  
GCTTTTTCAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180  
TTAAGGCGTT ACTTTACCAA CTAAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240  
25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGAATGATC 300  
TCTTGTGATT TCTTCCAGGT CCTAATTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360  
TTGCAAGATG GAATGAGAAG TGAAnACACGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60  
GGCATAAAAA AAAGAGACCT TCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTGCTT 120  
45 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180  
GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240  
TACTAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300  
50 GCCATTTTTC TTTGTGTnnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

- (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60  
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTTCGAT 120  
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AAAGTGAATG ACAATATGTC 180  
 15 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240  
 TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300  
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

20

## (2) INFORMATION FOR SEQ ID NO: 4294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

30 TTATCACCCA TGTCTGACT CCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60  
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120  
 35 GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTGCGATT GGAATTTCTC 180  
 CGCTACCCCTC AGTTCATCCG CTCACTTTTT AACGTAATCG GTTCGGTCCT CCATTCACTG 240  
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300  
 40 AAACGCCCTA TTCA 314

## (2) INFORMATION FOR SEQ ID NO: 4295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

55

GCAATCTATC TGTTGAAGAC ATTGATTTGA TCGAATTGAA CGAAGCATTT GCTTCTCAAA 180  
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240  
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300  
 TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60  
 GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA 120  
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180  
 ACTTTTGTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CgNACTACCA TCGACGCTAA 240  
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300  
 GACATATGAA TGThAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360  
 C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTCACTT CGCCAAGCCA 60  
 TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120  
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180  
 AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTTCGTCAGA TTCAAACGTT 300  
 TTCACTTCGC CAAGCCATTT ThCTTTGTGT nTACTnT 337



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

```

10 GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA      60
   CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAAC      120
15 GGAGGAAGAG GGATTGGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA      180
   TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC      240
   TGCAGCCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT      300
20 TTTTACAAC TATAAAATAG TGG                                              323

```

(2) INFORMATION FOR SEQ ID NO: 4299:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

```

30 CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG      60
   AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT      120
35 ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG      180
   GCTCTTTAAT TGTA AAAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC      240
40 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA      300
   ATCAACACGA GGAGATGCTA TTT                                              323

```

(2) INFORMATION FOR SEQ ID NO: 4300:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120  
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA 180  
 5 AAATACAAAT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240  
 GTTnCATTTGA AGTGTTTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTC TTGGACTGTG 300  
 CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360  
 10 GCTGAATGGC TnGnTGAAT GAATT 385

## (2) INFORMATION FOR SEQ ID NO: 4301:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GCGGACGTGA 60  
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 180  
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240  
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300  
 CTTCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

35 (2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

45 AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60  
 AGGTGTTATG AATGGCATAAC ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120  
 CAGAAGCAAG TGCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180  
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240  
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

55

TTTTGAGCGG CAAAACTTT GnCAG

385

## (2) INFORMATION FOR SEQ ID NO: 4303:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

15 AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTAAACGCA 60  
 GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT 120  
 TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGAC ACGTCATCTT TAACTTAATC 180  
 20 GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA 240  
 GATTTATGGG CACTTAAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA 300  
 TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA 360  
 25 CCAAGCCTTG TCCC 374

## (2) INFORMATION FOR SEQ ID NO: 4304:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA 60  
 40 ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA 120  
 ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAAT TGGCTATCAC CCTATCGCTG 180  
 45 GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTGTC AGCAAATATA GTTGTGTTGTA 240  
 TGCAAGATGC TTTGGTCTAT TCATTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA 300  
 TTAAACAAA CGTT 314

## (2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60  
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120  
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180  
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240  
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300  
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

## (2) INFORMATION FOR SEQ ID NO: 4306:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60  
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CGGTGATTAT 120  
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180  
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240  
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300  
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360  
 GAAAnAGATGG TCAAATTT 378

## (2) INFORMATION FOR SEQ ID NO: 4307:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGAATTGGGT ATTCCTCCAA AATTATATGG ACCTTGCAAG ACTCGAACCT GCGACCGAAC 60  
 GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTGTAAAT AATATGGTGG AGACTAGCGG 240  
 GATCGAACCG CTGGACCTCC TGCCTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300  
 5 CCATAATAAT TACAGTAT 318

## (2) INFORMATION FOR SEQ ID NO: 4308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA 60  
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTC CAATTAACCTC 120  
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180  
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTAC TTAATAATAC 240  
 25 TGTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300  
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360  
 30 CAATCCTATT GGATGTCCCA AnaATTGTAC GACCAACACC 400

## (2) INFORMATION FOR SEQ ID NO: 4309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60  
 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120  
 45 GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180  
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCATTG ATGACAATGG 240  
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300  
 TTCACACTAA TCAATGGTGG CAAAGT 326

## (2) INFORMATION FOR SEQ ID NO: 4310:

- (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTC AGTGATAATG 60  
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120  
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180  
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTCTCTAT 240  
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAc GGCATCATAA ATGGnCAATG 300  
 TCGGATCACT TTT 313

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(2) INFORMATION FOR SEQ ID NO: 4311:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

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GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60  
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120  
 35 TTGGGAAGTG CTTTTTTTAA GGTTCCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180  
 TATTTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240  
 TGGTTGTCTT CnTTTTTTCT CTTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300  
 40 GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TChATAGACC 360  
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

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(2) INFORMATION FOR SEQ ID NO: 4312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

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ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120  
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180  
 5 ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240  
 CTTTAAAATA ATTAACATCAT TGTCTGCAAA ACGTTTTCnT TTATAAAAAG ATTAAACGCG 300  
 TTATTAAACT GTGGAGTG 318

(2) INFORMATION FOR SEQ ID NO: 4313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCGG CCACCCCGGC 60  
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120  
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180  
 AAGGCATAGA TCCTAAGTCT AGTGCCTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240  
 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCn 300  
 30 AATGGnTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAC 60  
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120  
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180  
 50 TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240  
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300  
 GGCCATTGTA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGnCCAT TCCATG 356

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA 60  
 AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT 120  
 CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA 180  
 TGTCAGCGAA GGAATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA 240  
 TTGGTGTAC AATTATCCTT GGGGCCCTTT GCATATTCnG GGTTGTAGGG AATCAGGTCC 300  
 GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT 360  
 TGCCTCAGCG GAGGACACGC 380

## (2) INFORMATION FOR SEQ ID NO: 4316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT 60  
 TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT 120  
 GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT 180  
 ATTCTTTGTC CGTTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT 240  
 TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT 300  
 TGTGTCTCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AAACCTTATAA TCCACACCCT 360  
 GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn 400

## (2) INFORMATION FOR SEQ ID NO: 4317:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

5 CTTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60  
 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAAC TATAAGCAAA 120  
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180  
 10 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240  
 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300  
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360  
 15 CGGTGGGAGG TTAAGGAAT TTACGGGGAG GTTCTGGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 4318:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAAC TCTCTTTCT 60  
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTCTGGTC 120  
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTCGAT TCACCTGTAC 180  
 TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTTGGCGT CGTTATTGTC TTCTCACCTn 240  
 35 TTTGTCCTTC TCTTGTAAC TTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300  
 TTCTTGAAGG AATCTCTTC 319

## (2) INFORMATION FOR SEQ ID NO: 4319:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

50 AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60  
 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120  
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT 180

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ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300  
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCAC TTCG CAAGCCCATC TTTCTTTGGn 360  
 5 GTTTGCCT 368

## (2) INFORMATION FOR SEQ ID NO: 4320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60  
 20 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240  
 25 TCTACTCTAG CGGAANTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300  
 GACAATCGCT TGCTTCTTTT CCTCTCCTnG GGCTCTCGGT TAACTCA 347

## (2) INFORMATION FOR SEQ ID NO: 4321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120  
 ACTGCCGGTG ACAAAACGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 45 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAGGGCA GCGAAACCGC GAGTCaAGCA 240  
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300  
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

## (2) INFORMATION FOR SEQ ID NO: 4322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC	60
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAT GGTTTAGCAA	120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG	180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAATCCG TTTGGAAnGG AGCATCGAAA	240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGACT GGGGATATGT ATTCAGAGCC	300
CACGATCGTT TTGATGCATT TCAGTTCGGC	330

(2) INFORMATION FOR SEQ ID NO: 4323:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT	60
TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA	120
CTTGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA	180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA	240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTT	300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG	337

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(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA	60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG	120

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GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240  
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300  
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

## (2) INFORMATION FOR SEQ ID NO: 4325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAACTT 60  
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120  
 TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180  
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240  
 25 AGCACACGGT TTCAGGTTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTCCCTC 300  
 ACGGnACTGG TTCAC 315

## (2) INFORMATION FOR SEQ ID NO: 4326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60  
 CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120  
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180  
 45 AGACATATGA ATGTAAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240  
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300  
 ACCATGCTT 309

## (2) INFORMATION FOR SEQ ID NO: 4327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAAGA CGATATACTA 60  
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT 120  
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA 180  
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA 240  
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT 300  
TTTGGTTnCA G 311

(2) INFORMATION FOR SEQ ID NO: 4328:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT 60  
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT 120  
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 180  
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA 240  
CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG 300  
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA 340

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(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

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AATCCATAGC GAAATGTATA CCATCACCCA TGCCTCCTTC TAAAGGTAAA TCTCTACCTT 60  
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA 120

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TACGACGTCG AACCATCTT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240  
 CGCCTGATTG TCTAGCACGT TCATAAATAG TTAAGTTGTA TCCTnGTAGA TTAAGTTCTT 300  
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60  
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120  
 GATTGGAAT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180  
 ACCCTCCAT AAATGGTGCG GCGGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240  
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA 300  
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTCCACATT TGGAAAATT CTCCAGTAAC AATGAAAGAC 60  
 CATATACCTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120  
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180  
 45 TTGTTATTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240  
 AGTCATCATA TGCAGGTGGA TTAACAAAT GATGTTGTTT TACCAATGTC GTAATTCTT 300  
 GGATAGCCCG ATGGnTTAAA TTGTTAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360  
 50 GTTAAAAACG TCACGGACTT TGTTTAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60  
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120  
 AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180  
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCGAA 240  
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTATTTTTA CAAGGAACAT 300  
 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360  
 20 CAGGAT 366

## (2) INFORMATION FOR SEQ ID NO: 4333:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT 60  
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC 120  
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180  
 40 CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTCAC TTGCTGTGTT GGGGCCCTCA 240  
 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCCTGA 300  
 CTGAGAATTG GAAAAAGCT TGTGACAAG CGCnATTTTC GTTCCATGCA ACTGACTGCC 360  
 45 AAGAGAACTT CGTGAGAGCn ATGAAGAAGA TTGGATTGTA 400

## (2) INFORMATION FOR SEQ ID NO: 4334:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60  
 GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTTA 120  
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180  
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240  
 10 TGTTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATCCGCCA TCTTCTGnAA 300  
 GAAGATGTT 309

## (2) INFORMATION FOR SEQ ID NO: 4335:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60  
 25 ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120  
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTA CTGCGTC CCCCCATCGA TTAAACGAT 180  
 TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTG GnCTCAGCTT 240  
 30 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300  
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

## (2) INFORMATION FOR SEQ ID NO: 4336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGCA TGGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATT A GTTGGGCAC TCTAAGTTGA 120  
 CTGCCCGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180  
 50 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240  
 GCAAATCCCA TTAAAGTTGT TCTCAGTTG GATTGTAGTC TGCAACTCGG ACTACATGAA 300



## (2) INFORMATION FOR SEQ ID NO: 4337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

```

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT      60
TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCCATAAG      120
AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT      180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCATTATTT      240
TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AntGGCTnCT      300
CCCATCAGAG CTCAGCCTTA ACGA                                             324

```

## (2) INFORMATION FOR SEQ ID NO: 4338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

```

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG      60
ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAAT TGATTcGGTT GTTTGCTCAA      120
TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA      180
AGATAAGTCT AACAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT      240
ATTGGTAAAA ACACCCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC      300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT      360
GTGACGATAA TGATATGCGC CAGTAATAnt TTGTGnTTT                               399

```

## (2) INFORMATION FOR SEQ ID NO: 4339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 10 TATAGGCCCA TTTnTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240  
 GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300  
 AGCCGCACCT TCCGGATACG GCT 323

## 15 (2) INFORMATION FOR SEQ ID NO: 4340:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTCGAT TGAATTTCT 60  
 CCGCTACCTT CAGTTCATCC GCTCATTTTT CAACGTAAGT CGGTTCGGTC CTCCATTACG 120  
 30 TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180  
 TACTAAACGC CCTATTGAGA CTCGCTTTTC CTACGGCTCC ACATTTACTG CTTAACCTTG 240  
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTACGGG 300  
 35 CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

## (2) INFORMATION FOR SEQ ID NO: 4341:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60  
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120  
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180  
 AAGCCTCTAG ATAGAAAATA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

55

TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

15	AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC	60
	CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA	120
	CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
20	TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAnGA GCTTAACTTC TGTGTTCCGC	240
	ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT	300
	TCAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

35	ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA	60
	CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC ACACTGTTGA	120
40	AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTCAG GATTGTCACC TTAAAATAC	180
	GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
	CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT	300
45	TCCAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60  
 5 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120  
 GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAACT CTCGTGGTGT 180  
 10 GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240  
 CTAGCGATTG CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCT 300  
 TATGGGATTT GCT 313

## (2) INFORMATION FOR SEQ ID NO: 4345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60  
 25 AATAGTTTTA CTTTAAGTCC AGCATTCAACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120  
 CCTGCGCCAA GAACGGTTAC TTTATTAAAT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180  
 30 ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAAGTAT 240  
 CTTTGACAGT CATCTTAGCC TCTTATTAA GGnAAAAGCh TTATGCTTAA nATAAGTCTT 300  
 TTTTA 305

## (2) INFORMATION FOR SEQ ID NO: 4346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60  
 TTTTAAGCTT GAATTAAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120  
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TGAGCAAGT TGCTCAAAT 180  
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTGGA TGAnCAACGC CAACCAAAT 240

AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360  
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

(2) INFORMATION FOR SEQ ID NO: 4347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60  
 ATTCTGTAC CACCTATAAT CGTTTAAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120  
 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180  
 AAGGCTGAGC TGTGATGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240  
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300  
 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATT 60  
 TTTAGGTCTC GTAGTGTAGC GATTAACACG CTGCCTGTC ACGCAGAGAT CGsGGGTTCG 120  
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTTT TGCCTTTAAT 180  
 ATTATATTAA TAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTCGTCCA 240  
 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTh 300  
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

5 CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60  
 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120  
 TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC 180  
 10 CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCG AACCTCTGAC CCTCTGATTA 240  
 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300  
 CGAACCAACG AGTGACGGA 319

## 15 (2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

25 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAATGGTG GAGAATGACC 60  
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120  
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180  
 30 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240  
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300  
 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

## 35 (2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60  
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120  
 50 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG 180

55

ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300  
TGACC 305

5 (2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 302 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTCATCAAT TGCTAATTC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60  
CTTTAAAACC TGGCTTCTTT GGCTTTTTCG ATATAATGTT GCGATTGTTT TATTGTAAAT 120  
20 ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180  
GCAATCATTT CTTCTAAAAA TGCTCATTT GAACTTGCCT CTTTAGGTAC AGCATGAGGC 240  
CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACTTTC 300  
25 AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 411 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60  
TCCTAAGTCT AGTGGTCTG CCAATTCGCG CACACCCGCA AATGGTGAGC CATAGAGGAT 120  
40 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180  
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240  
45 CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300  
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CnTTTTAAAA 360  
CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

50 (2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 367 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

	TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa	60
10	CGACAACTGG TACACCAGAG GTATGTCCAT CCGGGTCCTC TCGTACTAAG GACAGCTCCT	120
	CTCAAATTTCTACGACCAC GACGGATAGG GACCGAACTG TCTCAGACG TTCTGAACCC	180
	AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA	240
15	GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAac TCTTGGGGGA	300
	GATAAGnCTG TTATCCCCGG GGTAACTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG	360
	GAAACCA	367

20

(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

30

	GTATTTTAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG	60
	TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT	120
35	TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT	180
	TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAaATT	240
	AGAGGAAATA CTAATTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACTT	300
40	GnCATTTGTCT GTT	313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

	GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATT	60
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55



TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180  
 GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 240  
 5 ATGAGGTTAA TAGGTTTCGAG GTGnGAAGCA TGGTGACAGT GGrAGCTGAC GAATACTAAT 300  
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

## (2) INFORMATION FOR SEQ ID NO: 4357:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGr 60  
 nGAACCTAAA AAAAGCACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120  
 TCGAACCTCT GACCTCTGA TTAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180  
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240  
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 300  
 AGAG 304

## (2) INFORMATION FOR SEQ ID NO: 4358:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

40 ATAATGGTGA CGTTGATGAT GCATTAAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60  
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120  
 45 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTAA GCATTAGCAA 180  
 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240  
 AAGTTGAAAA AGCGAACTC AAGGACTTGA AGCATTGAT AACATTCAnn TCGACTCAnC 300  
 50 AG 302

## (2) INFORMATION FOR SEQ ID NO: 4359:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60  
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120  
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180  
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCTGGGG CTGTAGTCGG 240  
 TCCCAAGGGT TGGGCTGTTT GCCCATTAAA GCGGTACAG GCTGGGTTCA GAACGTCGTn 300  
 AGAAAGTTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

20

## (2) INFORMATION FOR SEQ ID NO: 4360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

30 AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60  
 GGTGTGTACA AGACCCGGGA ACGTATTACG CGTAGCATGC TGATCTACGA TTACTAGCGA 120  
 35 TTCCAGCTTC ATGTAGTCGA GTTGCAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180  
 ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240  
 AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300  
 40 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

## (2) INFORMATION FOR SEQ ID NO: 4361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA 60

CTnTCCTCTC CTTGGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGGGCTCTTT 180  
 TCTCGTTTCG TCAGATTCAA ACGTTTTTTCAC TnCGnCAAGC CATTTTTTCTT TGTGTTTACT 240  
 5 TTTTATTTTG ACGTTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300  
 GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360  
 10 TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420  
 TCGC 424

## (2) INFORMATION FOR SEQ ID NO: 4362:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

25 CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60  
 CGTGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGGTA AAGAAACGCA 120  
 ATThAnTCGT TATTTCCGAC AAGAACGTAA CAATACTACA TACAACTTAG CACCATGAAT 180  
 30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240  
 AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300  
 TGGACAGCAG ATTCCA 316

## 35 (2) INFORMATION FOR SEQ ID NO: 4363:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60  
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTGG AAATCTCTGG ATCAAAGCTT 120  
 50 ACTTACAGCT CCCCAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180  
 AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240  
 55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

## (2) INFORMATION FOR SEQ ID NO: 4364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

```

nTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG      60
GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA      120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG      180
TGTACCTCAC GGCCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA      240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTTAGTACGT GGTATATATC      300
GTTCCAAAAA CGT                                     313

```

## (2) INFORMATION FOR SEQ ID NO: 4365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

```

AACCATTGCA TGCAATAGCG TCATTCTGG ATATTAATCC CTAAATTGCC GTGATATCCC      60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC      120
TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG      180
CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn      240
CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn      300
AGTCATTTTC                                     310

```

## (2) INFORMATION FOR SEQ ID NO: 4366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60  
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120  
 5 AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180  
 GTTACAAATT ATTTCAAGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTCAGC 240  
 10 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300  
 ACATTAAngG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360  
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG nAATTATAAA 400

15 (2) INFORMATION FOR SEQ ID NO: 4367:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60  
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCTT ATTTATCAAC GGTATATGAA 120  
 30 GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAACG 180  
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTGCAATGC 240  
 CGATGTTACT CGCnATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300  
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

- (i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60  
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120  
 CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180  
 55 GTGCATCATT TACACCGTCA CCAncCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

GTTTTGC

307

## (2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

15 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG 60  
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120  
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180  
 20 TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT 240  
 CCTACAGGAA ACGCGTTATT AATCTTGTA GTGTTCTTTC GAACATAGC GATTATTCT 300  
 TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA 360  
 25 TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA 396

## (2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

40 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 60  
 CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 120  
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTACATA 180  
 45 CTTTAAAAA ATAAGACACT TTGCCAACT TGCACATAAA TGTTAATTC AATAATTGA 240  
 ATTTTCTGTG TTGGGTCCTT TCGTATAATT TAATAAATAC CACTAAACTA AATTATGAA 300  
 GTGCCTTATG TATAA 315

## (2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60  
 CGTGTGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120  
 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180  
 10 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240  
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAATCA CCAGGGnCAC 300  
 15 CAAAATTTTT ATCGACGGCn TG 322

## (2) INFORMATION FOR SEQ ID NO: 4372:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CCTAAGTCTA GTGCGTCTGC CAATTCGGCC ACACCGCAA ATGGTGAGCC ATAGAGGATT 60  
 CGAACCTCTG ACCCTCTGAT TAAAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120  
 30 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180  
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTTCnA 240  
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300  
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

## (2) INFORMATION FOR SEQ ID NO: 4373:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60  
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120  
 AGTCATTAT GACATTGCTC AAGACAAAC TGCCGAATC GAAATTGAAA ATATTATAGA 180

TCAATTTTAA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300  
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360  
 5 GGNCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

## (2) INFORMATION FOR SEQ ID NO: 4374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTAGTGTTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60  
 20 TACTTTTCT GTCCCTGGTG CTAATCAGG ATTAAATTTA CGTTCTTCT CGAATGGAAT 120  
 CTCTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180  
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACCT 240  
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300  
 NCGTTTCTGG GTCCGNAAGT CTGTNGAATT GCAG 334

## (2) INFORMATION FOR SEQ ID NO: 4375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTNG TGAATGTTAG CGGCGGACGG 60  
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCCGGAAA CCGNAGCTAA 120  
 TACCGGATAA TATTTTGAAC CGCATGGTNA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180  
 45 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240  
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAACCT GAGACACGGT CCAGACTCCT 300  
 50 ACGGG 305

## (2) INFORMATION FOR SEQ ID NO: 4376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

	GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
10	AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TCGGATTCCCT GAAGTATTGT	120
	CACTCAGCAA TCTATCTGTT GAAGACATTG ATTGATCGA ATTGAACGAn CATTTGCTCT	180
	CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
15	GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
	CTTAA	305

20

(2) INFORMATION FOR SEQ ID NO: 4377:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

30	AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTgN CCTAATACTC	60
	AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT	120
	CCCCCATCG ATTAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
35	CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG	240
	GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
40	TCTCACTTCT AAGCGCTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

	CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
55	AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240  
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300  
 5 GGGAAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360  
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAATC 400

10 (2) INFORMATION FOR SEQ ID NO: 4379:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAATATA TCACTTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60  
 TTGTGACTGA GATGAACCTT TATGTCTTAG AACTACAAC ACTATATTGG CAGTAGTTGA 120  
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCAATTT CTACAGACAA TGCAAGTTGG 180  
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240  
 GTGTACTCAT GTTGCGATTA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300  
 TCGCTACATA ATCCATCCAT TAGGTCGTTC CTTGATTCAT TCCCT 345

30 (2) INFORMATION FOR SEQ ID NO: 4380:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60  
 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120  
 45 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180  
 CTGTGTTAAT TGGTCGTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240  
 50 AGATATGCTA TTATTCATGG AAGATTAGTG CTTTCATCTT TTTACCCCAA TATTTTATAA 300  
 GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360  
 ATn 363

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAACCTTG ACTTTnCGAC AATTGACTGT nCATTITGCA TAGTTGTATG 60  
 nCTCCATTnC GTAATTATTA GATTTGTTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT 120  
 ATAGTTAGCG TATTTGCACC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATT 180  
 TTAAGTAAAT TAAGGAATCT ATAATGTTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA 240  
 CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTTGGGAC 300  
 CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG 360  
 GCCGTTGTCA CTTAACTTCT GTTTTTCCGA TGACAGCTTC 400

## (2) INFORMATION FOR SEQ ID NO: 4382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTAC TGACGAATAC TGGCAATGAC 60  
 ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC 120  
 CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTCAG 180  
 TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTGCAATT 240  
 TGTTCITTCG TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT 300  
 AGGG 304

## (2) INFORMATION FOR SEQ ID NO: 4383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60  
 GCGGTTTCGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120  
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180  
 GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240  
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300  
 AGTTGGTA 308

## (2) INFORMATION FOR SEQ ID NO: 4384:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTCAGAGTG TCATTGGCAT TTATTACACT 60  
 25 ATCTCCAACCT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120  
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180  
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGkAGCTA CACCCTTTCC 240  
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300  
 TTTAGAnAT 309

## 35 (2) INFORMATION FOR SEQ ID NO: 4385:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

45 AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60  
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120  
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTCGTAGCC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240  
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

55

## (2) INFORMATION FOR SEQ ID NO: 4386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA 60  
 ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA 120  
 TGGCAAGGTC ATCTTCAAAA TGATTCGATT CAAGTGAAG GCATATGACG TCTCATCACT 180  
 ATACCCTTTT TCCCATTCG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC 240  
 CATTGCGGCGC AATCTCGGTh AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT 300  
 TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG 360  
 CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTChGGCAT 400

## (2) INFORMATION FOR SEQ ID NO: 4387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA 60  
 TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAAA TAATTTTACA 120  
 GTGTTTGAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTGTCTCTG 180  
 CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCnC 240  
 GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA 300  
 TGGATGACGA 310

## (2) INFORMATION FOR SEQ ID NO: 4388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTGAGGTTA 60  
 5 CTA CTAGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120  
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180  
 10 TGA ACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240  
 TTA CTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300  
 TTG GCGTGG 310

## 15 (2) INFORMATION FOR SEQ ID NO: 4389:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

25 TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA 60  
 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120  
 TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180  
 30 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTAA TACAGTTGGC TCTGGTGATA 240  
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300  
 35 CA 302

## (2) INFORMATION FOR SEQ ID NO: 4390:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGC TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60  
 50 ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120  
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180  
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

55

TnCCCTTACCA CCTATAATCG nTTAATCGTG GGG

333

## (2) INFORMATION FOR SEQ ID NO: 4391:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

15 AGTGCGTTTG TGCACaNACT TGACTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG 60  
 GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA 120  
 TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG 180  
 20 CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT 240  
 ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC 300  
 AACCAT 306

## 25 (2) INFORMATION FOR SEQ ID NO: 4392:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

35 TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTATT AGGACATATA AATTCATCAT 60  
 TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT 120  
 40 TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAAATCA TCTATAATAG 180  
 CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAATAAC 240  
 CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT 300  
 45 GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTTGCCnC AATTnGTAAA TGGAA 355

## (2) INFORMATION FOR SEQ ID NO: 4393:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 364 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTCAGG TTTCTTCTTT GCATTTGGTG 60  
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120  
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180  
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240  
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300  
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTAnTAAC GATAATGGCG 360  
 15 nngg 364

## (2) INFORMATION FOR SEQ ID NO: 4394:

20 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60  
 CGGCCTCAGC TTAGGACCCG ACTAACCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120  
 30 GTCAATCGGT GGACGGGATT CTCACCCGTC TTTCGCTACT CACACGGCA TTCTCACTTC 180  
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCC TTAGAAGCT CTCCTAnCAT 240  
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTA GCCCGGTAC ATTTTCGGCG 300  
 CATGTnCACT CGACT 315

## (2) INFORMATION FOR SEQ ID NO: 4395:

40 (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGACTCG AACCACCGAC 60  
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120  
 ACAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

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TACGACTTCA CCCCAATCAT TTGTCACACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300  
 ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120  
 GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA 180  
 GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTG ACAATCGCTT 240  
 GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT 300  
 CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTTCTATA AAATTTTTC 60  
 ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120  
 GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180  
 GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAAAGTCA GCAACAAGCT GAATTACATA 240  
 AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300  
 TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360  
 GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TCnATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
40	ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 409 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TC GTTGC GCT CTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
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AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180  
 TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 300  
 ArATTCAAAC GtTTTCaCTT CGGCCAAGGC ATTTTTCTTT GTGGTTACTT TTTAATTGG 360  
 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409

## (2) INFORMATION FOR SEQ ID NO: 4401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60  
 ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120  
 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180  
 TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240  
 TGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300  
 TCCATATTTT C 311

## (2) INFORMATION FOR SEQ ID NO: 4402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60  
 AAGTCAGTCG CTAAGATTG TGAAAGTAGA TCGGAAATT GGTTTAAGCA AACTGTTGCA 120  
 TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180  
 AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240  
 TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAACAGA AAATTAAAGC 300  
 AGGTCCATGT nAAGTGTTGG CGGGnCGCAT 330

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

10

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC	60
TTTGGGCCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT	120
TACTTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC	180
AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT	240
TTTGAGGTGG TACTTGATAT AAATTTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA	300
TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTTG	340

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## (2) INFORMATION FOR SEQ ID NO: 4404:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA	60
CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTGGGAG TTTGTCTGAA	120
TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AACAGTGCT CTACCTCCAA TAATCATCAC	180
TTGAGGCTAG CCCTGAAAGC TATTTCTGGGA GAGAACCAGC TGATTTCCAG GTTCGATTGG	240
AAATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC	300
TGCCATT	307

40

## (2) INFORMATION FOR SEQ ID NO: 4405:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

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AnACTTGAGT GCAGAAGAGG AAAGTGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120  
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180  
 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240  
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300  
 CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAACACG TATGGAAGAC GAACTTGGAG 60  
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120  
 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180  
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAGTAAA AATAATGTCA 240  
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300  
 ACnChAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCATC ATAAAATAGG TGGACAGGAA TATCAACCTG 60  
 TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCGA CTAACCCAGA GCGGACGAGC 120  
 CTTCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180  
 CACCGGCATT CTCATTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240  
 AGAACGCTCT CCTACCATTG TCCAAAGGAA TChCACAGCT TCGGTAATAT GTTTAGCCCC 300  
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG 60  
 TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC 120  
 ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA 180  
 TGTGTTAGAT ATTACAGCAG CACATTTATC TCGCGAAAGT CCCAGCTGTC GATAAAGGTT 240  
 GAAACTGAAA AACGGATTTC TGGATTTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG 300  
 AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAATTTGG AATCCAAATC nnTTACCAGG 360  
 TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC 393

## (2) INFORMATION FOR SEQ ID NO: 4409:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTG TGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 60  
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 120  
 GCCATTTTTT TTTGTGTTTA CTTTTIATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT 180  
 TCGCGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 240  
 AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCTTG ACTTGTGGAC AATCGCTTGG 300  
 CnTCTnTCCT CTCCTTCGG 319

## (2) INFORMATION FOR SEQ ID NO: 4410:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAATAACGC CTAACCTCGT TAACTTTTAA 60  
 AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTCGGTAA 120  
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180  
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240  
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAAGTACGA CCAGTTTTTC AACTGAGCAC 300  
 10 AATTGTGCAC ATCGATTGGT GACAG 325

## (2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60  
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120  
 TGAAATGACG ATAGAGTCAG TATTAAGTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180  
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTnGGCA nGTATGTTGT ATTACCGTTC 240  
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTAA TTGGCCATTC GGGTAAGTTG 300  
 TCCGACCATT GCCAAGTGGG TGATGAGTTn AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360  
 TCCGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

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## (2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60  
 CCCGAGCACA TTATTTATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120  
 50 GAATGATAAT CGAACGTCAT ATTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180  
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA 240

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CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360  
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

15 TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC 120  
 20 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180  
 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA 240  
 GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC 300  
 25 TTGCGTCCTT nCCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

35 GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCAGTA CCGTGAGGAA 60  
 AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120  
 40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTTGTAGA ATGAACCGGC GAGTTACGAT 180  
 TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240  
 45 TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300  
 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60  
 TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT 120  
 CTCAAATGCG GTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAATA 180  
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240  
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTh 300

## (2) INFORMATION FOR SEQ ID NO: 4416:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGna ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60  
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120  
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TAGCACCAGA AAATACAGAT TGAGTATATG 180  
 30 CATATAAGAT GATTTTAAAC ATCATCTTTG GATGATAGGA TGTTGCGCCA CGATGATGTC 240  
 TGAATTCATC GAATTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

## (2) INFORMATION FOR SEQ ID NO: 4417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60  
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA 120  
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180  
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTC AAGCAAATA 240  
 TGTAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

GTTTGGTGGG ACGnATTGGA nGATAACCAT GGATAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 4418:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAATAAG CAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60  
 CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120  
 GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180  
 CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAncATCGA AATGGTTTATG TAACTCATAC 240  
 AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

(2) INFORMATION FOR SEQ ID NO: 4419:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60  
 CCTACCATTG TCCAAAGGnA TGCnCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120  
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180  
 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240  
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

(2) INFORMATION FOR SEQ ID NO: 4420:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120  
 AGGGGTGCTC TTTAGGTTAA CGCCAGAAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180  
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCG 240  
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAACT ACGAATCGAA GCCCCAGTAA 300  
 10 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

## (2) INFORMATION FOR SEQ ID NO: 4421:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 297 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60  
 AAGCTATTTTC GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCTC 120  
 25 AGTTCATCCG CTCACTTTTC AACGTAATCG GTTCGGTCCT CCATTCACTG TTACCTGAAC 180  
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240  
 30 TTCAGACTCG CTTCGCTAC GGCTCCACAT TTA CTGCTTA ACCTTGCA TC AAATCGT 297

## (2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60  
 ATTCAACGAT GCCGTTGAAG CGGTAAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTCTG 120  
 45 GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180  
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240  
 50 CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCAa CAATAGAATG 300  
 ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360  
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 291 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACTAT CAAGCTTTGA 60  
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120  
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180  
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240  
 ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGGTAGT T 291

## (2) INFORMATION FOR SEQ ID NO: 4424:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnC GTTTCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60  
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120  
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTGTCATGAG CATTTTTATn CAGTAATGGG 180  
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240  
 GCAACATTTT TACCTAAATC AGCGGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300  
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360  
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

## (2) INFORMATION FOR SEQ ID NO: 4425:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTTTTGGCA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120  
 ATATATTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180  
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240  
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAATCGAAT 300  
 10 CCATTtTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

## (2) INFORMATION FOR SEQ ID NO: 4426:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAAATTACG GATCATGATG 60  
 ATTTCACTACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120  
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTCAG 180  
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240  
 30 ATAGCGACTC AGATTCAGAT AGCGATTCAG ACTCAGACAG CGACTCAGAT TC 292

## (2) INFORMATION FOR SEQ ID NO: 4427:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60  
 AACCAGCTAT TTCCAGGTTT GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120  
 45 TTCAACGTA ATCGGTTTCG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180  
 TAGATCACCT GGTTCGCGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240  
 50 CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300  
 ATTCTAn 307

## (2) INFORMATION FOR SEQ ID NO: 4428:

55

- (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60  
 TTTTtagcag CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTAT ACGAGATGGT 120  
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGACGTCC ATCTGGTGAA GTGAAGGCAT 180  
 15 ATCTTCTTCA GGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240  
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAa GATGATTATT ACACGTnACT 300  
 AATTGGTTTA CACCAGGTGG AnAATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

20

## (2) INFORMATION FOR SEQ ID NO: 4429:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTGTTTTAAA AGATATTAGA 60  
 CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120  
 35 TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180  
 GTGCACATTA TTAaAATATC AATTTCACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240  
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300  
 40 GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTCGGCTCT CGCTTACTCC ATTTAGCTCC 360  
 ACTAAACTCG TCGGGCCCTT CCCGTTTCGGC AGATCCAACG 400

45

## (2) INFORMATION FOR SEQ ID NO: 4430:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

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ACCATTTCACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120  
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180  
 ATCGATAGCG TTTTGCGCAA ATTCTTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240  
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 284 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60  
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120  
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180  
 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240  
 TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCCGCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT 60  
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120  
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180  
 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240  
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300  
 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

	CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
10	TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
	AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAG AACTCGGCAA	180
	AATGACCCCG TAACTTCGGG AAAAAAGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC	240
15	AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 336 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

	GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC	60
30	AATCGAACCT GGAGATAGCT GGTTCCTCTC nAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
	GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCT CTCGGGTAC CAATTCAGA	180
	CAAACTCCGA ATGCCAATTA AATTAACTT GGAATTCAG AACATGGGTG AThAAGTCCG	240
35	TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA	300
	AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

50	ATTGACGCCG CATTTTTIACG GAATGGGAAT AAACGCACAC AAACCGTCAC GTCnGTGTTG	60
	GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
	GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTGCTT ATTCAGGCAC	180

55



AATCATTGGC TGCCTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGATTTA 300  
ACGA 304

5 (2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60  
CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120  
20 ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCA TATGGTCTTC CTTCAATTCTC 180  
ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT 240  
TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACCTCT 300  
25 TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 359 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60  
40 TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120  
TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180  
AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA 240  
45 AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300  
GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTGTAAAA 60  
 CATAAACCTT GnAAACGGCA ACATTTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC 120  
 ATTATGATCA ATATCATGCC CAATTAACCT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180  
 10 ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240  
 ATCTTTATTA ACAATTGCTT CATCATTAATA ATGTGAGATT AAATCG 286

## (2) INFORMATION FOR SEQ ID NO: 4439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

25 TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60  
 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTCT 120  
 TTGTGTTTAC TTTTATTTT GACGTTTtag ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 TGCGGCTCAT CGCATCCATT TTTTGCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 240  
 30 GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTTCCTCn 300  
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 360  
 35 TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT 394

## (2) INFORMATION FOR SEQ ID NO: 4440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

45 TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60  
 GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120  
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG 180

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn

295

## (2) INFORMATION FOR SEQ ID NO: 4441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60  
 CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120  
 TAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180  
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240  
 TAAATAAACA TTCAAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300  
 TGTTCGGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

## (2) INFORMATION FOR SEQ ID NO: 4442:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCAC 60  
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120  
 CGTCATTGCT CAAATCATTG ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180  
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCA TCGTTAACAT 240  
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTG GTATATCACA AATTTGTAGT 300  
 GTATCTTGGA TGC 313

## (2) INFORMATION FOR SEQ ID NO: 4443:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTATGTTT TAATTTTTC 60  
 5 CAGTCTTTAA AAATAGATTG TTTATTTTGA GAATTATTTT TGAATAATTG AATTGCTTTG 120  
 TAGCCAAAAT ATGACGTTTC ATTATCAATC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180  
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240  
 10 CTGAAACCCC ATTCCCTTTG AGCTGCCCCAT ATATCTCTTT GGACAATATC GGTCCTCTA 300  
 ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTT 336

## (2) INFORMATION FOR SEQ ID NO: 4444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTC AGAAATGGCA AAAGACTATT 60  
 25 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120  
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGGAAGGG TGAAATTGAA GCGGTACCTG 180  
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240  
 ATGTCACGCT TGGGCCTGTA CTTGAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300  
 35 TCCGTGTCCA GTTGAACCAT TATGGAGGAn TTnAAAAAGT ATGTTAAGGG ACCTGGGAGT 360  
 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

## (2) INFORMATION FOR SEQ ID NO: 4445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60  
 50 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120  
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTTGA CCCTGACTAC GGACTTGTnA GGTCTGCGGC ATTCAAGCTT 300  
 CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTTG 339

5 (2) INFORMATION FOR SEQ ID NO: 4446:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTGAAAAT GTCACTTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60  
 CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120  
 20 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT 180  
 CATTGTAAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240  
 ATAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300  
 25 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60  
 40 TTTTATTTC A GTCAACTACT AACAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120  
 ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180  
 TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240  
 45 GTAAAAAATG AACGATCAAT GGTnTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60  
 5 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120  
 CCCCAGGTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180  
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT 240  
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTCTGnA TTGAACACGG 300  
 GA 302

## (2) INFORMATION FOR SEQ ID NO: 4449:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAATGTG GACACAGTTT TTACAAGAGG 60  
 25 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120  
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180  
 30 TACAAAACAA TGAnACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240  
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300  
 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

## (2) INFORMATION FOR SEQ ID NO: 4450:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60  
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAA CAATACTTTT ATAGGGCAAC 120  
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180  
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTCAAGCT 240

GCTATACGGT AGAACGACTT ATTCCC

326

(2) INFORMATION FOR SEQ ID NO: 4451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

15	GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA	60
	TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT	120
	TCAACAACCTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA	180
20	AGACAACCAA GCCCAATAAT GGACTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT	240
	TTAAAAATAG GTCTTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAACCAT	300
	GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA	360
25	TAAAGCGGGG GGCAATTGGG G	381

(2) INFORMATION FOR SEQ ID NO: 4452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

	TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT	60
40	CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC	120
	TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT	180
	CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA	240
45	AATAAACATT CAAAACTGAA TACAATATGT CACATn	276

(2) INFORMATION FOR SEQ ID NO: 4453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTTAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60  
 5 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120  
 AAATGCGCAG AGATATGGAG GAACACCAGT GAGCGAAGCG ACTTTCTGGT CTGTAAGTGA 180  
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240  
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AGTGGCTGCC AGCTAaACGC 300  
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAaNTTG A 341

## (2) INFORMATION FOR SEQ ID NO: 4454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60  
 25 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 120  
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180  
 30 TAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240  
 TATTAATCTT GTGAGTGTTT TTTCGAACAC TAGCGATTAT G 281

## (2) INFORMATION FOR SEQ ID NO: 4455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60  
 45 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTTCTACT 120  
 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 50 GCTTGcNTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240  
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60  
 CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180  
 ACTCATTAG CTCTACTAAA CTCGTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240  
 nTCACTTCGC CAAGCCATTT TTCTTGTTT TACTT 275

## (2) INFORMATION FOR SEQ ID NO: 4457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60  
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120  
 TTCGGTAAGC ACATCAGCGT CATTAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180  
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCCTCA ACATCACTCA GTGACTCAAC 240  
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300  
 AnTGAATCC GATTGTGCGT CAACATCTTT AAGTGGATTC AACATCTGCG TcATGCCAA 360  
 AGnnGTGAAT CCGATTCA AAGCACATCA GCATCCTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120  
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180  
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240  
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTTCGG 300  
 10 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

## (2) INFORMATION FOR SEQ ID NO: 4459:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60  
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120  
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTThACAATA 180  
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240  
 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

## (2) INFORMATION FOR SEQ ID NO: 4460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120  
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180  
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240  
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

## (2) INFORMATION FOR SEQ ID NO: 4461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG	60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC	120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC	180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTAAAAT CAACAAnCAT AACTTTCCnG	240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC	274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA	60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA	120
TGATGGACGT ACAGGTGAAC CATTCGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT	180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT	240
TGnTACACAA CAACCACTTG GCGGTnAAGC G	271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCATTT CTTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
TACCATCCTC GCTAAGAAC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC	180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTAnTTTGAC	240

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## (2) INFORMATION FOR SEQ ID NO: 4464:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60  
 TTCCTTGTCTG GGTAAATTCC GACCCGCACG AAAGGCGTAA CGATTGCGG ACTGTCTCAA 120  
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180  
 GAAAGACCCC GTGGGAGCTT TTA CTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240  
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300  
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360  
 G 361

## (2) INFORMATION FOR SEQ ID NO: 4465:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAG TATAAATTCA 60  
 ATCATTCCGA AAGAGAAATG GGTAAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120  
 AAGGTGCTAT TCCTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180  
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240  
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGT TTTTnTTTT TT 292

## (2) INFORMATION FOR SEQ ID NO: 4466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60  
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120  
 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180  
 GATAGTAATG CATTAAAGTA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240  
 10 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300  
 AATAnTGG 308

## (2) INFORMATION FOR SEQ ID NO: 4467:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGAAGAC 60  
 25 AGGATTGCGA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAAngCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240  
 30 GAATCGAACC GGTACGTGAT CACTCACC GC A 271

## (2) INFORMATION FOR SEQ ID NO: 4468:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TGCCTCAAAG TCCAGCTGTC GATAAAGTTG 60  
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120  
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180  
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240  
 50 AACGATTAAC TGGTATTCCA GTTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA 300  
 ATATTT 306

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

10 GGTTTATTAA CAGCATTCTT ATCAGCATTT GTAACGTGTA TTGTTTATAA CTTCTGTGTG 60  
 AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTC ACAAGTATTT 120  
 AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT 180  
 15 CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240  
 ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTTAACnT TGGGnGCnTT TGCATTAAATC 300  
 20 CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

## (2) INFORMATION FOR SEQ ID NO: 4470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

30 AACTGGGTGA TAAGTCCTG TTCGAAAGGA AACAGCCAG ACCACCAGCT AAGGTCCCAA 60  
 AATATATGTT AAGTGAAAA GGATGTGGCG TGCCCGAGAC AACTAGGATG TTGGCTTAGA 120  
 35 AGCAGCCATC ATTTAAAGAG TCGTAATAG CTCCTAGTC GAGTGACACT GCGCCGAAAA 180  
 TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240  
 40 CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300  
 TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360  
 GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

45

## (2) INFORMATION FOR SEQ ID NO: 4471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

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TCATTTTITAG AAATATTATC TTTTCCACAA ATCATTTGAT ATAAAGTGGC ATCATTTGCC 60  
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC 120  
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180  
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240  
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCTCC GTTTTnCATG TACCGCGAGG 300  
 10 CGTAAnCTTA AAGGGCCCAA GGnCG 325

## (2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60  
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120  
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180  
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240  
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

## (2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60  
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAaGAATA GATTGTCAAG CGCTCGCATA 120  
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 180  
 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240  
 50 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCAT 300  
 TGTCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60  
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGCC GCAGGCACAA TGGGCGCTCA 120  
 ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAaNA CTATTAGATA TTGTAGTGGA 180  
 CAAAAACGAT CcNaATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240  
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTACCAT ATGGTATTTT GATGTGCTTG 300  
 GTAAATGTGT GCTGTTTGAT ATCGA 325

## (2) INFORMATION FOR SEQ ID NO: 4475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60  
 CAATACATCT AGTATTATCT GGTATTTTGT ATCGTTATCC AAAGTTAAAT AATGATTATT 120  
 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180  
 GACATTThAC CACCCTGTAA GCTATACITT AAAAATAATT TTTAATCACA CCGAGTGGCA 240  
 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300  
 TGATATCC 308

## (2) INFORMATION FOR SEQ ID NO: 4476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:



CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120  
 GGGTCTTTCC GTTCCTGTCG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTACCCGA 180  
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240  
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60  
 CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120  
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180  
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240  
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60  
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAATGG TCCTCCACCT TGAGCTTCTT 120  
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180  
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240  
 GGAACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

EP 0 786 519 A2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

	GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA	60
5	GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA	120
	ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC	180
	AAGCGCATT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA	240
10	TTTATGTCCC AGCCTGAGTT AATTT	265

(2) INFORMATION FOR SEQ ID NO: 4480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

	ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA	60
25	ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACCTAA CTTCTTGTTT TTCCGATGAC	120
	AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG	180
	TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT	240
30	ATATTCCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT	300
	TTCATAGTGG TTCCAATTAA ACCAntCTTC AGGAACCTCh TAG	343

(2) INFORMATION FOR SEQ ID NO: 4481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

45	ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC	60
	GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA	120
50	AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT	180
	ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT	240

## (2) INFORMATION FOR SEQ ID NO: 4482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTCAAA GTTTGGTGGT AAACCTGnTA 60  
 CATCAAATTA TCGGTGCTAC TGnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120  
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180  
 ATGGGGATTG GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240  
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

## (2) INFORMATION FOR SEQ ID NO: 4483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60  
 TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120  
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180  
 CATTTAGCTC TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240  
 ACTTCGCCAA GnCATTTTTTC TTG 264

## (2) INFORMATION FOR SEQ ID NO: 4484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180  
 nAAGCCTCTA GATAGAAAAA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240  
 5 AATTCTAAGG TGAGCGAGCG A 261

## (2) INFORMATION FOR SEQ ID NO: 4485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60  
 20 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120  
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180  
 25 GATGGANTAA ATCTTTTAAG GCTTATAAAC GTCATCTGA CATTGTAGAN GTCATGCTTT 240  
 CAAAAGACGA TATACTACGA C 261

## (2) INFORMATION FOR SEQ ID NO: 4486:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAAACTTG TAGACATACG 60  
 40 TAAATCTGCT TTAATAAGTA ATtATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120  
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGANTTTGAG CGCCTTGCTT 180  
 45 TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240  
 TACCGTTGAT AAATAAGTTA 260

## (2) INFORMATION FOR SEQ ID NO: 4487:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60  
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120  
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTGTTCTT CATATTTATT 180  
 10 TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACTTC TTAATCTTAG TTCTTTTTTA 240  
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTCCCCCA ATAGAATGAA TTAAACCTT 300  
 CCGATTTCTT TTAAnC 316

## (2) INFORMATION FOR SEQ ID NO: 4488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

25 CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60  
 TCAAAAAGTT ATAGAAGAAG CTACTAAAGT TAAAACAGAG ATTGATACTG CCAGAAGATA 120  
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180  
 ATTAAACCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT 240  
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300  
 35 GACTCAA 307

## (2) INFORMATION FOR SEQ ID NO: 4489:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60  
 50 GTTCCCCAAT CATTAAATTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120  
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAAGTGGC 180  
 55 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240

TAGCAGTATG CCACnCCGn GACGATATGG TAGCGACGTA AnAA

344

## (2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

15	CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCTGTC	60
	TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT	120
	TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA	180
20	TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA	240
	CAGGTACTnA GTAACTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG	300
	TTCATTTGAC CGG	313

## (2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

35	AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT	60
	ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCAAA TGAGCCAGAA CGTGATGAAG	120
40	TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG	180
	AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA	240
	AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnCh A	291

## (2) INFORMATION FOR SEQ ID NO: 4492:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

5 GCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60  
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAACACT TTGCCCACT 120  
 TACACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAT GATATTTTCG GATATGTTAA 180  
 TGAAATTGTT AAAAGATAG CTGATAGCGA GATTTCGATGG AATTCAGACA TCATCGTGGG 240  
 10 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300  
 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360  
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGcT 400

15 (2) INFORMATION FOR SEQ ID NO: 4493:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60  
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120  
 30 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180  
 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240  
 ACGAATCATC TGGAAAGGTG AATCA 265

35 (2) INFORMATION FOR SEQ ID NO: 4494:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60  
 TAAGGAAGAG ATTTCTTGA AAGAGCTTGA TTTTAAATG AGAAAACAAC TTATTGAAAA 120  
 50 ACATAATCTT TACGGTAACA TGGGTTTCAGG AACRAATCGTT ATTAAAATGA AAAACGGTGG 180  
 GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG 240  
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60  
 ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120  
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180  
 GCATTTAACA GCATTnAAAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT 240  
 AGGAGCAAGC AGTGCA 256

## (2) INFORMATION FOR SEQ ID NO: 4496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTCA CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60  
 TTCATCATTa TCTAATTTAA AACAAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120  
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AnATACCCAA TATACTTTTT 180  
 ATATCGTTTCG GATTCTGAGT ATTTCAGACG ATTTTCTGCA TAnAAATAAA CGTGTTTCAA 240  
 GGCAATATAT TGCA 254

## (2) INFORMATION FOR SEQ ID NO: 4497:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGnTATCTGA ATCCGAGTCG 60  
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120



GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240  
 TCACTGTnGG AATCTGAATC GCTATCTGA 269

(2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG 60  
 GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120  
 CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180  
 AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240  
 CCAACTGAGC TAAATGGCTC TnCAAGGTGC CGG 273

(2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60  
 TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120  
 TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180  
 TCAACGAAGG AGACAAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240  
 AGCAAGTGGA GGAATTCGAA GTTGTTCAAn CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300  
 AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60  
 5 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120  
 ACTTAACTTT AATGGCGGTC GTCATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180  
 CCATTTATGC TGTTAAAAGG CCGTATAGCT GATAAAGTAT GGnCTGATTA CCGTGGCGGT 240  
 10 AATTCTATAC AAATTAGGAC CCGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300  
 CATT 304

## (2) INFORMATION FOR SEQ ID NO: 4501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

25 TTCCTTCATT CTCATAAAG TTGCATCATG ATCAGATCAG TTTAGAAAA ACTATTTCTA 60  
 TCTTTAAGAA TCGATTTTTG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT 120  
 TTCTTTTGA ACTTCTTAAT CTCAGTTAAT TTTTACGGG TCTGTTTTCT AATTGAGCA 180  
 30 CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240  
 CAATTAAATC TAT 253

## (2) INFORMATION FOR SEQ ID NO: 4502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

45 AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG 60  
 AGGACCGGGA TGGACATACC TCTGGGTGAC CAGTTGTGCT GCCAAnGCAT AGCTGGGTAG 120  
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCCC CAAGATGAGA 180  
 50 TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240  
 AGCATGGTGA CATGTGG 257

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 270 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60  
 TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120  
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180  
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA 240  
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60  
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120  
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180  
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240  
 TACCACCnGn T 251

(2) INFORMATION FOR SEQ ID NO: 4505:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60  
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGA<sup>n</sup>CTTGTA<sup>n</sup> TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC 240  
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 313 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60  
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120  
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180  
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240  
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAATCGG CTGTGGGTAT 300  
TTTGGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60  
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120  
GCTGTTAATT TACCATCAGG TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180  
GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240  
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTACTCG CACTTGTGTA GTCTGATGTT GAATCACTAA CACTATCAGA 60  
 5 TAATGACGTT GAATCACTCA TACTTGTGTA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120  
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180  
 10 TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA 240  
 10 ATCGGATTTC GCTCGTGCT GGTACTnG 268

## (2) INFORMATION FOR SEQ ID NO: 4509:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 296 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60  
 25 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCCACGCTT 120  
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180  
 30 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240  
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA 296

## (2) INFORMATION FOR SEQ ID NO: 4510:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60  
 45 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120  
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAAT TGTCTTACTA 180  
 50 TGTGCTGCA CCATTACCCA CTTnTTCACT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240  
 TAATTAAATG GTCCTGA 257

## (2) INFORMATION FOR SEQ ID NO: 4511:

55

(A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

10 AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAGTATCT 60  
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120  
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTTTAAAT CATCCATAGC AATTCTCGTT 180  
 15 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240  
 TGATAAATGC 250

## (2) INFORMATION FOR SEQ ID NO: 4512:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

30 AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60  
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT 120  
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180  
 35 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240  
 CTCTCCCCAG CTG 253

## (2) INFORMATION FOR SEQ ID NO: 4513:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

50 GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60  
 nAAGTTACGT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTGC AGTGTTCCTT 120  
 CGAACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

55

GTGGAGACTA GC

252

## (2) INFORMATION FOR SEQ ID NO: 4514:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 244 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

15 GTCATTGAAT ATGGAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG 60  
 ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC 120  
 TCTTGCAGAA CAGTTAAAAG ACCATTTTAC TGTGTAGCC GTTGATCGTC GTGATTATGG 180  
 20 AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCTGACA GTGATTATCG 240  
 TGTC 244

## (2) INFORMATION FOR SEQ ID NO: 4515:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

35 TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT 60  
 TCGAGTCGTT GATTTACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC 120  
 CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA 180  
 40 AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC 240  
 CCA 243

## (2) INFORMATION FOR SEQ ID NO: 4516:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

55

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120  
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180  
 5 CCGTCCACCG ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240  
 CCCTAAACCT GAGGCCGCAA nnGTAGG 267

## (2) INFORMATION FOR SEQ ID NO: 4517:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60  
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120  
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180  
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAT 240  
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300  
 GAACGAGAAA GAGCGCACG 319

## (2) INFORMATION FOR SEQ ID NO: 4518:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

40 GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60  
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAATTT 120  
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180  
 CATGTCAAnG TACCATTGTC AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240  
 ACATGAAAAA CGGGGAACA 259

## (2) INFORMATION FOR SEQ ID NO: 4519:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	- 60
10 CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15 TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 245 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AATCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCnACC ATCGTCGCTA	180
AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35 CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 251 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT GGACTCGAAC CACCGACCTC ACGCTTATCA GCGGTGCGCT CTAACCAGCT	60
50 GAGCTATAGG CCCATTAAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
55 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT	240

## (2) INFORMATION FOR SEQ ID NO: 4522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60  
 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 120  
 GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG 180  
 TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240  
 ACGTTTGAA 249

## (2) INFORMATION FOR SEQ ID NO: 4523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60  
 GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAng CATAGCTGGG TAGCTATGTG 120  
 TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180  
 CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240  
 GACAGTGG 248

## (2) INFORMATION FOR SEQ ID NO: 4524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGA<sub>n</sub>CGGCT GTGGCTCG<sub>n</sub>A 180  
 CCAATACGGG TCGGACCTGC TThAACCATT TTATTGAAA TCTTCTAAAT TACGGACGGC 240  
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCA<sub>n</sub>TTAAT TTAACGGCTT 300  
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

## (2) INFORMATION FOR SEQ ID NO: 4525:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

20 AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60  
 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120  
 TAGAGGTTTT CTGGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180  
 25 GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240  
 CGCAGTTnGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300  
 C 301

## (2) INFORMATION FOR SEQ ID NO: 4526:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

40 TGATATTATG AGCTGTGTTT TTAGCTTTAG AACC GAAGTC CCCTGCTTTT TTACCAAGAT 60  
 TTTCAGTAAC TTGTnCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTGGCAAAA 120  
 45 CACCCATCCG CTGTAACTTC AGAGTGTCT TGGCATTTAT TACACTATCT CCAACTCCTA 180  
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240  
 T 241

## (2) INFORMATION FOR SEQ ID NO: 4527:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

	CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10	TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
	ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
	TCGCAACCAT nCAATCATCT GGCAGTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15	GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
	ATACCACCCA ACACCT	316

20

(2) INFORMATION FOR SEQ ID NO: 4528:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30	GTCCCAAGGG TTGGGCTGTT CGCCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
	GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
	TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35	CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
	AAGATGAGAT T	251

40

(2) INFORMATION FOR SEQ ID NO: 4529:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 318 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50	AGTACGTGAC GTTCACTACT CTCCTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
	ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
	TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

55

ATGGTCGTTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300  
 GTGACGCGAC AGTGTcNA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60  
 GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120  
 20 GAGCAAAGAn GATGTTCTnc GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180  
 CAAGTGCCGT CTGCCAAAAC GGTAAGTAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60  
 35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG 120  
 TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180  
 40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GChCAGCCTT AACGAGTACC 240  
 GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

55

EP 0 786 519 A2

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120  
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180  
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60  
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120  
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180  
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240  
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTC AATT TTTAAACGTA TTATTTTCATT 60  
 40 GAGCAGAAAG AAAATTATGG CACCAAACTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120  
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTC GTCGTCCAC CCCAACTTGG 180  
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240  
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

5 GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60  
 GACGCATAGG NATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120  
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180  
 10 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240  
 AAACCGACAC 250

## (2) INFORMATION FOR SEQ ID NO: 4536:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

20  
 25 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60  
 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAANTAA TTCGAACTAC 120  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 30 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

## (2) INFORMATION FOR SEQ ID NO: 4537:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

40  
 45 TGCATCTTCA CAGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60  
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120  
 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTTCGTAGC TTCGCAGAAG CTAACCACTC 180  
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

## (2) INFORMATION FOR SEQ ID NO: 4538:

50  
 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGTnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAAGTGC 60  
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120  
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180  
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240  
 TA 242

## (2) INFORMATION FOR SEQ ID NO: 4539:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60  
 TATTGCGTTT GGTCTGTCGT GCCAGTGCAA GATTTCACAC GATAATTTCT AGGCGTCACT 120  
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180  
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

## (2) INFORMATION FOR SEQ ID NO: 4540:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60  
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120  
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180  
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240  
 50 AT 242

## (2) INFORMATION FOR SEQ ID NO: 4541:

55



(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 15 GnAGTGTTCT TTCGAACATA GCGGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

## (2) INFORMATION FOR SEQ ID NO: 4542:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60  
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GCGGAGGnTG ATGAATGCCT TACGTTTGCG 120  
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGTAAT GGCATACTGA GCTGACGATT 180  
 ATGATATTGT CAGTTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240  
 35 TG 242

## (2) INFORMATION FOR SEQ ID NO: 4543:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60  
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120  
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180  
 55 GAnTGACGGG TTCGAACCGC CGACCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAGTCAG ATGCTCTACC AACTGAGCTA 60  
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120  
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180  
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

## (2) INFORMATION FOR SEQ ID NO: 4545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60  
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTATTAA TCGTTTAAAT TCAGTTAGTA 120  
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAATA TTATAGAAA CATCAAAGGA 180  
 TGTTAAGAAA TACnATTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

## (2) INFORMATION FOR SEQ ID NO: 4546:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60  
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTGC TAnTTTTTCA TGTGCTTCCG 120  
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180  
 GTTCAACTTG GncGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

## (2) INFORMATION FOR SEQ ID NO: 4547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60  
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120  
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180  
 AAGAAGTTTA AACCGBAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240  
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

## (2) INFORMATION FOR SEQ ID NO: 4548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAACTAGA TAGTAAGTCA 60  
 AAGTGATTTT GCTTCGCAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180  
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240  
 GGCTTTnCAG CACTTTATGC CCGGnCCAC ACATTAGGCT TACCCAGCCT ATGCCCCGTTT 300  
 GGCACG 306

## (2) INFORMATION FOR SEQ ID NO: 4549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120  
 ATAAAGATTC AATTAACGCA TCAGTATTAG GATTCACCTCT AATACGATTA ATAGTTTTAT 180  
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTCGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60  
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120  
 CGTGCCAAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180  
 AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC CCTCAAAGAT 240  
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60  
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCAATTT TACAGACAAT 120  
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTCTGTn CCCTCCCTCA 180  
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTCTGCT CATGAATATA 240  
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300  
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360  
 50 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTACTTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGAG AGAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTG GATTTCATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

(2) INFORMATION FOR SEQ ID NO: 4553:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAATA CCAATACCA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGTTTCGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAAGTAATT GCTAAATGTG GnGAATTTCT	240
	CCAGTAACAA TGGA	254

(2) INFORMATION FOR SEQ ID NO: 4554:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

55

CTGGGGCTTG G

251

## (2) INFORMATION FOR SEQ ID NO: 4555:

5

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

15 TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60  
 ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCCA ATGATTTAAG 120  
 AGGGAACATG GATGCGAGTG AATTCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180  
 20 CTATCTGAAA AAGCCCAACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240  
 AGAAGCATGG C 251

## (2) INFORMATION FOR SEQ ID NO: 4556:

25

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

35 AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG 60  
 GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120  
 TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180  
 40 TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240  
 ATA 243

## (2) INFORMATION FOR SEQ ID NO: 4557:

45

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

55

TCATTATTTT AAATGCTCAT TTACATAAGT AACTCTGCT TTAAAATAAT TTAACTCATT 120  
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180  
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTAAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60  
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120  
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180  
 ACGTGTTTGA TCACCCAATT TAATGATTTC ACGCTTGTC AATAATnATT TTCGAGACGA 240  
 25 GAGGATCGGA TTAAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60  
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120  
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180  
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAATTA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120  
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT 180  
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

## (2) INFORMATION FOR SEQ ID NO: 4561:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60  
 TCACTCCCCT TCCGGGGTGC TTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120  
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCAGATT CCGACGGAAT TTCACGTGCT 180  
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240  
 CTTTGATTCA TCTTGTC 257

## (2) INFORMATION FOR SEQ ID NO: 4562:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60  
 GCCACAATTA CCATACCAAT TTTCTTTTTC TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120  
 TTAGCTCCGA TTGAAACGAT GTCTTGGTTT ACAGGACTAA CAGCCATTC AGTTTGACCA 180  
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

## (2) INFORMATION FOR SEQ ID NO: 4563:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

5 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60  
 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTA 120  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGTCAT TTACATAAGT 180  
 nGACTCTGCT TTAAATAAT TTAACTCATT GTCGCTAAA CGTTT 225

10

## (2) INFORMATION FOR SEQ ID NO: 4564:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60  
 ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120  
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAATTACG GTGGTTACAA 180  
 AATTATTTCA GGTTCCTTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT 233

30

## (2) INFORMATION FOR SEQ ID NO: 4565:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

40 AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60  
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120  
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTTCAG 180  
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

## (2) INFORMATION FOR SEQ ID NO: 4566:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

5 CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60  
 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120  
 TGGAGANTGA CGGGTTTCGAA CCGCCGAnCC TCTGCTTGTC AAGGCAGATG CTCTCCCAGC 180  
 10 TGAGCTAATT CTCCGATTTA AAAGTGGCCT GGGCAACGTT CTACTCTAGC GGGAAGT 237

## (2) INFORMATION FOR SEQ ID NO: 4567:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

20 GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60  
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120  
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAAC ACAGCTCATA ATATCAAAAA 180  
 GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240  
 TAAATCGCGA TGTGTGGGTT AntACACATC CGGGAAGTAG TAATAAGTAT GTCAGTTTAA 300

## (2) INFORMATION FOR SEQ ID NO: 4568:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

40 ATCCCGTGGA GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60  
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTTCA TTCCCATCAC 120  
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180  
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240  
 AAACATTCCA 250

## (2) INFORMATION FOR SEQ ID NO: 4569:

## (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTT AACTTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60  
 10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120  
 AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180  
 TCAGATTCTG ACCCAGGTTT AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

25 AATCIATTTT TTTATTTGTT AAATCGCTAT CTCCATCTTC TTTATCTCT GGTATTATTT 60  
 TTTCITCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTT GATTCGTGAT 120  
 30 TTTGAATACT TTTCTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180  
 CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

45 CATGATATTT TGAACCGCAT GGTTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60  
 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120  
 CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180  
 50 GGCAGCAGTA GGGAAATTTT CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240  
 TGCTGCAGGT TCTTCGGATC GTAAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

55

(A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTA CTTACTA TCTAGTTT T AATGTATAAA TTACATTCAT ATGTCTGGTG 60  
 ACTATAGCAA G G nGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120  
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180  
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60  
 30 TTCGGTGCAn TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120  
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CTnAGAGGGG AATTGCTTGA TCAACACAAG 180  
 GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAATG 230

35

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

45

TCACATATCG ATAACATGAC ATA A C T C A T G C T G G G T T T C C C A T T C G G A A A T C T C T G G A T 60  
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120  
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATA A C T T A A T C n A T G T T T C C A C C A T T T T T A 180  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

55

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60  
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120  
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180  
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240  
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300  
 CCTTAAATT 309

20

## (2) INFORMATION FOR SEQ ID NO: 4576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30

TGATTCTAGG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60  
 ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAA TAATGGTGGG CCTAAGTGGG 120  
 35 CTCGAACCAC CGACCTCAGC CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180  
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

## (2) INFORMATION FOR SEQ ID NO: 4577:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60  
 TGGGTAAAAA TnTATTAATT GGGTGGTTG TGAAATGCAA TCTTTTTAAC GACTTCAGGG 120  
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

55

## (2) INFORMATION FOR SEQ ID NO: 4578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT 60  
 AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC 120  
 CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTT TTTTGTAGCA ATGAGTACGC 180  
 GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAACTG ACATACTTAT 240  
 TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300  
 CTTGATTACG CGCGCTCAAC ATTG 324

## (2) INFORMATION FOR SEQ ID NO: 4579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAA CTGATTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT 60  
 GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG 120  
 GTATGCATAT CGTTTAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAT 180  
 TCGTCATATT TCCAATTTTG AGTGTA AAAA ATGTCACTTT TAACTTTC 229

## (2) INFORMATION FOR SEQ ID NO: 4580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA 60

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180  
 CGTAAGTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTGGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAGAGAG ACAACATTTT 60  
 CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTGCTC TAATGTCGTC 120  
 CTTTGTAAC TCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180  
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60  
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120  
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCanCT 180  
 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGAAA 180  
 TAGGTCATAG GGTnAAAACh TTTTGAGAA TTGTCGCTA TTGTTAAAT TGTATCCCGG 240  
 5 CTTGAAGTTG G 251

## (2) INFORMATION FOR SEQ ID NO: 4584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTGTA GCTTCGCAGA 60  
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120  
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180  
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

## (2) INFORMATION FOR SEQ ID NO: 4585:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60  
 TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120  
 40 CTATATTAC TTAATTATCT AGTTTTCAAT GTACAATTnC TTTTtagTCA AGCGCTCGCA 180  
 TACTGCTnTA TTTTCAAAA ATCAAATGCT CATTTACA 218

## (2) INFORMATION FOR SEQ ID NO: 4586:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:



GGAATTCAC TTTCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120  
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180  
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCAGC TATTnAGCCG 240  
 T 241

10 (2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60  
 TGAAGTGAAT AAGAAATCAA TCATTGCTC TTCTGTAAA TCATGTGTTT TTTCTAATTT 120  
 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGGTTGCAC AAATAATACC 180  
 25 CATCGCAGCA TTGACTTCAT TGTGCAAGG CACnTTGAC TCGGCAATC ATTCATATCC 240  
 GACnAAGCAG ATG 253

30 (2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60  
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120  
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180  
 45 GGACGTACCA GTAGAAAAGG CTTTGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

5   GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTTAACAGC CGATAGCTCT   60  
 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA   120  
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT   180  
 10   GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA   216

## (2) INFORMATION FOR SEQ ID NO: 4590:

## (i) SEQUENCE CHARACTERISTICS:

- 15   (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

20   AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC   60  
 ATCnCATTCa TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT   120  
 25   CCTCGGCTAA GAACCTTTCT TGACTTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG   180  
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT   234

## (2) INFORMATION FOR SEQ ID NO: 4591:

## (i) SEQUENCE CHARACTERISTICS:

- 30   (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 35   (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

40   AATTGACTGA CTCGTTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC   60  
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT   120  
 TTCGTCGTCC CACCCCAACT TnCACATTA TTGTAACCTG ACTTTCGCC AGCTTCTATG   180  
 45   TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG   216

## (2) INFORMATION FOR SEQ ID NO: 4592:

## (i) SEQUENCE CHARACTERISTICS:

- 50   (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55   (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

5 ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTh TTAGCCGTGG 60  
 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120  
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGhTGCTCC GTCAGGCTTT 180  
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

## (2) INFORMATION FOR SEQ ID NO: 4593:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

20 TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60  
 AGCTTTGATC CAGAGATTTT CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA 120  
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180  
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

## (2) INFORMATION FOR SEQ ID NO: 4594:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

40 CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60  
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120  
 45 TAATCGAAGG TGTTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180  
 TTATCGGTTT AGGTGCCACA GnaAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240  
 TAATTTTTTT Th 252

## (2) INFORMATION FOR SEQ ID NO: 4595:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60  
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120  
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180  
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240  
 GTTACCCGGG AGnAAAGG 258

## (2) INFORMATION FOR SEQ ID NO: 4596:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCACTAG GATCTGCCCG TGCCGCACGT 60  
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120  
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180  
 TnCATTTGTTT AGTTGGGTAC ATTAATGCnG TATTATCGAC ACTACATCA 229

## (2) INFORMATION FOR SEQ ID NO: 4597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60  
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120  
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180  
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTCGCCTAT CCTACTGnGG TCCCCCATC 240  
 GATTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4598:

- (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60  
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120  
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180  
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

## (2) INFORMATION FOR SEQ ID NO: 4599:

- (i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60  
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAAATGACA TCTTCAATCA 120  
 TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180  
 CATCATCAGG TCITTCGTGG AATAATGCGC CTGCTTTGC 219

35

## (2) INFORMATION FOR SEQ ID NO: 4600:

- (i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60  
 CGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120  
 50 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180  
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

55

## (2) INFORMATION FOR SEQ ID NO: 4601:

- (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60  
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120  
 CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGcNAG 180  
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240  
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

## (2) INFORMATION FOR SEQ ID NO: 4602:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60  
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120  
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180  
 35 TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240  
 nTTAAACGGG GTATTAATCT TGTG 264

## (2) INFORMATION FOR SEQ ID NO: 4603:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60  
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120  
 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnc TAGTGATTAT TTACAACATG CCAAAGAATT 180

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TATCCn

246

## (2) INFORMATION FOR SEQ ID NO: 4604:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

15 ATTAACCTAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60  
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAA GGTGTATGGA 120  
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180  
 20 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240  
 TTTGATGG 248

## (2) INFORMATION FOR SEQ ID NO: 4605:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

35 CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTTGAGCCG GGACTTnTCA CATCAGACTT 60  
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120  
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180  
 40 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTnG TTTTGTnTTn 240  
 TGGGTT 246

## (2) INFORMATION FOR SEQ ID NO: 4606:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120  
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180  
 5 TGCAGTTATT TCAGTTTCTG CTTACGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60  
 20 GACCCCGTAA CTTCGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCAGAGAG AGCCGCATGA 120  
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180  
 AGGGGCTGAC GCCTGCCCCG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240  
 25 GGAATCGAAG CCCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60  
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120  
 GCTTCAAATG AATCAGCTGC TTTACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180  
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



GGGTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTGTG CGATTTTTTTA AATCGAATCG 60  
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120  
 GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTAAAC GCTTTTAAAT 180  
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCnGA ATnGATTAGC 240  
 C 241

## (2) INFORMATION FOR SEQ ID NO: 4610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120  
 TTAATCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180  
 TTTCAntTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

## (2) INFORMATION FOR SEQ ID NO: 4611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60  
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTIGATA AATATGGCGT GCGTTTGGCA 120  
 ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180  
 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240  
 TAAATTATCT TGTGATTGAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300  
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360  
 GGTCTCTACC TTCAGAACCG CTCATATCC ATCCTGTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60  
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120  
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180  
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG 240  
 ACCGTTAAGG TThAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60  
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120  
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180  
 35 AGCTTTTTTC TACAGCTTTT ACAATATThn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60  
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120  
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180  
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTAAAnTTTA 60  
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120  
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG 180  
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

## (2) INFORMATION FOR SEQ ID NO: 4616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60  
 TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120  
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180  
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

## (2) INFORMATION FOR SEQ ID NO: 4617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTTCT 60  
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120  
 ATGTATCAAC ATATCGCGGT ATGTTTAAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180  
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

## (2) INFORMATION FOR SEQ ID NO: 4618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCAh 60  
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 120  
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180  
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

## (2) INFORMATION FOR SEQ ID NO: 4619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60  
 GCGATThGTC GTCCTAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120  
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180  
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

## (2) INFORMATION FOR SEQ ID NO: 4620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAATT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60  
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120  
 CATTTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

## (2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

15 TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60  
 TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120  
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180  
 20 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTTnTGGnTTA CAGGTACGGC AGAACGATAC 240  
 ACAGTCTCGG GCGATTGTCTG AGTCCAC 267

## (2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

35 CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60  
 TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120  
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180  
 40 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

## (2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA 60

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180  
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240  
 5 AGCCTTCTAA ACCAGTGGA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300  
 A 301

(2) INFORMATION FOR SEQ ID NO: 4624:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20 CGAGGTGCTG CAGAAGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60  
 GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120  
 25 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180  
 TTTGAAAAAG GGGnAAATCA TAATCATtng GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

40 TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60  
 CTGAGTACGA CGGAGCACGT GAAATTCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120  
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180  
 45 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240  
 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300  
 A 301

(2) INFORMATION FOR SEQ ID NO: 4626:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60  
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120  
 10 CATTAAATCCC ATTTTANCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180  
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

## (2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

25 TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60  
 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120  
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180  
 30 AAAAAAAGA CGGATTAAATT ATCCGCTTTT TCCTTATATC T 221

## (2) INFORMATION FOR SEQ ID NO: 4628:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

40 ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60  
 45 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120  
 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180  
 TCCACCACAT GTTAAATATG CAGCAGAG 208

## (2) INFORMATION FOR SEQ ID NO: 4629:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60  
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GACTAACTA AAGTTCGTGC 120  
 ACACAATAA GATTGATCAG CTAAAGCTTA CTTCAAATA AAGAGATATA GCCATTAGTA 180  
 10 ACGTTAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240  
 TTGATACTnt ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300  
 CACTG 305

## 15 (2) INFORMATION FOR SEQ ID NO: 4630:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60  
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120  
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180  
 CAGCTCCACA TGTCACCATG CTTCAnCTn GAA 213

## (2) INFORMATION FOR SEQ ID NO: 4631:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60  
 TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120  
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180  
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

## (2) INFORMATION FOR SEQ ID NO: 4632:

55



- (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAATTT ATTCGAACCA TTATTTACAG 60  
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120  
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180  
 15 TCGAAGCGAA CTTCAAGTTG CTTC 205

## (2) INFORMATION FOR SEQ ID NO: 4633:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60  
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120  
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180  
 CTAATGTGTT AAGAACTACT ACAT 204

35

## (2) INFORMATION FOR SEQ ID NO: 4634:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TG TAGGTAAG 60  
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGCCTTACGT TAGCCCGTCT GATGTAGAAG 120  
 50 CTTTGTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180  
 AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55

## (2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60  
 GAAGAGTTGT TGAATCATTTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG 120  
 AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG 180  
 15 GCTTAAGTTG GCCATTTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAA GTAGACCTTG 60  
 30 CCGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120  
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180  
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

(2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CCGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA 60  
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCTT GAGAGGGTGA 120  
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180  
 TTCCGCAATT GGCgAAAGCT GTACGGGCAA CG 212

55

(2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60  
 TTTTITAGGG ATTTATGTCC CAGCCATTTT TGTATTCTATA TTTAAATTTT GATAATTTTT 120  
 CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTGA GATTAACCAA AATTAATATT 180  
 15 TACATTTCTT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240  
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCCT 60  
 GAGAAGTTTA AAATTTTATA TGTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120  
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCGG TAAATGCTA 180  
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60  
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120  
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180  
 55 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTAAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60  
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120  
 CGCTGAAC TA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180  
 ATCCTAAGTC TAGTGCGTCT GCCAA 205

## (2) INFORMATION FOR SEQ ID NO: 4642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60  
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120  
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180  
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTATGTn CCCAG 235

## (2) INFORMATION FOR SEQ ID NO: 4643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60  
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120  
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180  
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

## (2) INFORMATION FOR SEQ ID NO: 4644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60  
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120  
 ATTTATTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180  
 GTTGGGGGCC CGCGGGCAAG GtNACTAGAA TGAAAAAGC CTGTTACAAG CGATTTTCGG 240  
 TTCAGTCCAC TACTGGCAAT ATAACCTGTA GAGCTAGGAC ATTGG 285

## (2) INFORMATION FOR SEQ ID NO: 4645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60  
 CGCTTGtTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120  
 TACGAACGTG TTAAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180  
 ATTTAGATGG TGGCTTTTGA TAAACA 206

## (2) INFORMATION FOR SEQ ID NO: 4646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60  
 CTTACGGATC ATGATGATTT CAACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTcGnGA TA

222

## (2) INFORMATION FOR SEQ ID NO: 4647:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

15 GTACTATTCTG TGTGTGACAA TGTTCTTCCA GCATTGCTT AATGAATGCT TTTTCTTCGT 60  
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120  
 GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180  
 20 CCGAAATTAA TGACAGTCCA 200

## (2) INFORMATION FOR SEQ ID NO: 4648:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60  
 35 ACGCAGGAnG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120  
 AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTAA 180  
 TAAGCTTGGA ATTCATTAAG A 201

40

## (2) INFORMATION FOR SEQ ID NO: 4649:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGAATAA ATCTTTTAAG GCTTATAAAC GTCATCTGn CATTGTAGCA 60  
 ATTCATGCTT TCAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

55

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT

218

(2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

15	GTGGCGGTGC GACTGTCAGA AGCACGTTAA ATTAATGAAA GATACAGTAG GTGCTGATGT	60
	AGAAGTAAAA GCCATCAGGT GCGGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG	120
	CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG	180
20	ATTCnGATTA CTAATATnTA TG	202

(2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

	AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG	60
35	AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC	120
	TTGCTGTAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC	180
	CAAGGCAACG ATGCATAGCC GACCTGAGA	209

(2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

	TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG	60
	ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT	120

CCACTTATCG TGGTTGGAGA CA

202

## (2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60  
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAAGT CAAACGCTCT 120  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180  
 AACCGGTACG TGATCACTCA AChGn 205

## (2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60  
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120  
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180  
 AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240  
 CTATTAATCC ACACGGGTGA GAnG 264

## (2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60



AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180

AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

5 (2) INFORMATION FOR SEQ ID NO: 4656:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60

GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120

20 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180

ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

35 TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTGGG GGCTTAGCTC 60

AGCTGGGnAG AGCGCTGCT TTGCACGAG AGGTCAGCGG TCGATCCCG CTATCTCCAC 120

CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAATA TAGATTTTAC CAAGCAAAAC 180

40 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTGGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

55

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180  
 AAAAn 185

5 (2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60  
 GGGAGTACGA CCGCAAGTGT ATAACTCAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120  
 20 GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180  
 AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

25 (2) INFORMATION FOR SEQ ID NO: 4660:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

35 ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTTAAAGTCA 60  
 CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120  
 GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT 180  
 40 GATAGAAATC ACTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240  
 ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300  
 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360  
 45 CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTT TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60  
 5 CCAATTCTCC TnATGTTGGG GCCCCGAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120  
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180  
 10 ACATGAAATT TTTCCAAGTG ATATATTTT 209

## (2) INFORMATION FOR SEQ ID NO: 4662:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60  
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120  
 25 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180  
 CGCACCTGGT GTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240  
 30 GCCTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4663:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60  
 TTAAGGAAGC GATTACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120  
 45 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180  
 AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

## (2) INFORMATION FOR SEQ ID NO: 4664:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs  
 55 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60  
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120  
 GTAGCTCAGC TTGGTAGAGC ACTTGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC 180  
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

## (2) INFORMATION FOR SEQ ID NO: 4665:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 196 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACTT 60  
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120  
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180  
 30 CATTTTTGCA CGAATT 196

## (2) INFORMATION FOR SEQ ID NO: 4666:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

40 CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTCT 60  
 TAGATTGTGG TTTTTAGTT GGTGCCATGC TTTAACCTTT TCATTGATTT CAATAACAGG 120  
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180  
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTC 226

## (2) INFORMATION FOR SEQ ID NO: 4667:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAA<sup>n</sup>AA CCGGTGATCT ACCCTTGGTC 60  
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120  
 10 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180  
 CGAAATA 187

## (2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTCTT 60  
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCAGTCTG AACGCGATTCC CATAACGGA 120  
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATG<sup>n</sup> 180  
 30 TT 182

## (2) INFORMATION FOR SEQ ID NO: 4669:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTAAAAACA GTTACAACAG ATGA<sup>n</sup>AATGG 60  
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTGG AGACACCATC 120  
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180  
 TT 182

## (2) INFORMATION FOR SEQ ID NO: 4670:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCGATACC TAGGAAACCA ACTGGCAATG 60  
CACCTTTTAA AGTATTACGT AATGTTGTGT TCGGTTTACA TCTTACCCAA AGTGCTAATG 120  
CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180  
10 ATTGG 185

## (2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60  
25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120  
GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180  
30 CATTGAGACC GCAAGGnTnT 200

## (2) INFORMATION FOR SEQ ID NO: 4672:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCCGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60  
45 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTTCGC CATTAAAGCG nACGnTGCTG 120  
GGTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180  
TGTCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCTG TGCCACGCAT 240  
50 AGTGGGTAGT ATGTGTGGAC G 261

## (2) INFORMATION FOR SEQ ID NO: 4673:

(i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTcAGGTTG 60  
 10 AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120  
 ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180  
 CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTGAGAAA 60  
 GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120  
 30 CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180  
 AAGCTCCACG GGGTTCTTTC CGT 203

(2) INFORMATION FOR SEQ ID NO: 4675:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60  
 45 AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120  
 GGATTGGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180  
 50 TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTAA 229

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 178 base pairs

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTa TTACCTCAAT ATGCTTGTCa 60  
 10 TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120  
 TTACAAATTT AGTGTGCnGA GCGTCITTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60  
 25 TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120  
 TGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180  
 30 AAATCCCAAT CGAACCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240  
 GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAAa 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTa TGGAGCGGAA GATAGGTTTA 60  
 45 CACCTATACC TCGTTCGGGA AGGAnTGTTc TAAAAGTGAA CTACTCCCGC AATATTAAAT 120  
 ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180  
 50 AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACh 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACCTT 60  
CGCCAAGCCA TCTTCTTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG 120  
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60  
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAGAAG AAATCACAAA AGATCCCATT 120  
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180  
CCC 183

30

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60  
AGATGGTCCT CCCAGATTCC GACGAATTTT ACGTGTTCG TCGTACTCAG GATCCACTCA 120  
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180  
TTCGTCTAAT GTCGTCCTTT GTA 203

50

(2) INFORMATION FOR SEQ ID NO: 4682:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

5 GGGTCACACC TGTTC CATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60  
 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120  
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180  
 10 ACAAAGA 187

## (2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 187 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

20 GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60  
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120  
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CCGTGCGATT 180  
 TTAAATT 187

## (2) INFORMATION FOR SEQ ID NO: 4684:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

40 AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60  
 AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120  
 45 AGCTTATTTA AAACCTTTTA TTCACTCGGT TTTGTAAAAT CTATATTT 168

## (2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 168 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

5 ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTGGA 60  
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120  
 AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

## (2) INFORMATION FOR SEQ ID NO: 4686:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

20 ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60  
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120  
 25 ATTATTTTCA AAAAATCAAA TGCTCATTGA CAAAAGTAAA CTCCGCTTTT AATT 174

## (2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 166 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

35 TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60  
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120  
 40 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 189 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

50 AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60  
 55

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180  
 GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60  
 GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTAC TGCGGCTCTT 120  
 CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180  
 CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCGG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60  
 GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGA TTATGTGCAA 120  
 TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAn AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60  
 TTAAAGGGGG CCCAATTTTT CCCAAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240  
 TTAAGGGAAT TTAATAAATT TAAGGCCCTC CCCTAAATTA AATTAAAGG TGGGAAAAAA 300  
 5 AAAATTAATT AAAnAACCCA TTTTTTTTTT TTAATTTTAA ACCCAAAGG GGGTAATTG 360  
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60  
 nTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120  
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180  
 25 AAATAGGAAT ACATGAGTAA AACTCantGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA ACTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60  
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120  
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180  
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

GCACATTAAc CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60  
 CATGTGACCG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120  
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180  
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

## (2) INFORMATION FOR SEQ ID NO: 4695:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTCTTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

## (2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

35 AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60  
 ATACGTATCG TCAGACAATT TATGTCAATC CAGTGGAGA TAACGTTATT GCGCCGTTT 120  
 40 TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A 161

## (2) INFORMATION FOR SEQ ID NO: 4697:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

50 CCAAACCTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

15

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60

TTGGGCGTAA ACGCGCGTAG GnGTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120

GGGTCAATTGG AACTTGAAA CTTGAGTCAG AAGAGGAAGT G 161

20

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

30

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60

TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120

35

GGGCAAGGTC ATCTTGCAAA ATGGATTGCA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180

TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG 240

CGGACGCh 248

40

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

50

CCCAGCAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60

GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

55

## (2) INFORMATION FOR SEQ ID NO: 4701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60  
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCCTGCA GGCATATGCA CCGAAAGCTT 120  
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

## (2) INFORMATION FOR SEQ ID NO: 4702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 120  
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

## (2) INFORMATION FOR SEQ ID NO: 4703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60  
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120  
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60  
10 ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120  
GGCAACGTTT TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60  
25 AATGCCAATT AATTAACTT GGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAA 120  
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAAATATA TGT 163

30 (2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

40 TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60  
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTTG ATTGGCTGCA GTCGCGATGG 120  
45 TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTCGACn GTACCCGTCA GATATCCGCA 180  
GCAATGCAAT GTTGTGCAAG TTT 203

(2) INFORMATION FOR SEQ ID NO: 4707:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCACAGA GGAGGCTCGT CCGCTCTGGG 60  
 5 TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120  
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

## (2) INFORMATION FOR SEQ ID NO: 4708:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60  
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120  
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

## (2) INFORMATION FOR SEQ ID NO: 4709:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAACAA CCTAAGCAAC ATGTAGGCCG 60  
 TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120  
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

## (2) INFORMATION FOR SEQ ID NO: 4710:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

50 GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60  
 55

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

## (2) INFORMATION FOR SEQ ID NO: 4711:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

15 TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60  
 TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTGAG AATCTTTTTC 120  
 AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

## 20 (2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

30 ATAGTGAACC ACTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60  
 CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120  
 35 TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

## (2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60  
 CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120  
 50 CCTGGGAGAT AGCTGGTTCT CTCCG 145

## (2) INFORMATION FOR SEQ ID NO: 4714:

55

- (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60  
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120  
 AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

## 15 (2) INFORMATION FOR SEQ ID NO: 4715:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60  
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120  
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

## (2) INFORMATION FOR SEQ ID NO: 4716:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60  
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTGT TTGTAAAAGT GGCATTCTTA 120  
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

## (2) INFORMATION FOR SEQ ID NO: 4717:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGANT AAATCTTTTA AGGCTTATAA 60  
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA 120  
 CGAACTTGTC CAAGGATTAC GAAA 144

## (2) INFORMATION FOR SEQ ID NO: 4718:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60  
 20 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120  
 CTTAACCCAA CATCTCACGA CACGA 145

## (2) INFORMATION FOR SEQ ID NO: 4719:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60  
 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGA ATGGTGTCGT 120  
 40 ACACnATGCC ATTAAAAAT AGCATACCGG CAAAGC 156

## (2) INFORMATION FOR SEQ ID NO: 4720:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTGTTACGT ATCGACCGGT GGCTAACTAC 60

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60  
 TTAATTAGCT TAAACGCGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120  
 TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGCGCT AAGTAAATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60  
 CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120  
 TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCATTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60  
 GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120  
 AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

(A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60  
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120  
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCC CTCAAGATGA nATTTCCCAA 60  
 CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120  
 30 GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAATA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60  
 45 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120  
 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180  
 CAGCATGCCG GTGTTCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240  
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

10

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60  
AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120  
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

25

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60  
TGACAATTAA TAAAGAACCG TTCTTGCGCG AGCACAATGG GCGCTCACTG GCAGACTTTT 120  
GTGATGCTGA CTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

40

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA 60  
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120  
GCCCTCCCAT ACCTCGGG 138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCCG ATTTGTCTGA ATTCGTAACC 60  
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120  
 AAAGTATTTT GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180  
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60  
 AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCTAT CCGTCGTGGG CGTAGGAAAT 120  
 TTAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

## (2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60  
 ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGCAGTGGG nACAGCAAAT GATATTTTCG 120  
 ACAAATTTA TTTGTCGTC CCACCCAAC TTG 153

## (2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCAACTTGC ACATnATTGC 60  
 AAGCTGACTT TTCGTCACCTT GCTTTGTGG GGGCCGCCA ATAAGCGTTG TAGTGCCTAG 120  
 TACTTTGATT GATGTCCAAG TT 142

## (2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCTGA TTTGCAGAC TGATAAATCG CTTCAAGAAT 60  
 TTTTGTAACCT ACCATTGCTT GTTCCGTTT CAACTGGT TCAGTATCAT TTACAACnGC 120  
 ATCAATCCAA GCTTTTG 137

## (2) INFORMATION FOR SEQ ID NO: 4737:

- (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCGTTTAG TATTTGGTCG TACACGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60  
 AGTTCAGGTA AACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAT GAGCGGATGA 120  
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15

## (2) INFORMATION FOR SEQ ID NO: 4738:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25

GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60  
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120  
 30 GAACATGGTG ACATGTnATC TGCTTTTCTA ATCATAC 157

## (2) INFORMATION FOR SEQ ID NO: 4739:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40

GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60  
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120  
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

## (2) INFORMATION FOR SEQ ID NO: 4740:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

5 TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60  
 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120  
 TTCACTTCG CCAAGCCATT TTTCTTGTTT TTATTTTATT TGACGTTTAG ACATAAAAAA 180  
 10 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

## (2) INFORMATION FOR SEQ ID NO: 4741:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

20 GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GCGCATTAC CAGAGTTGCA 60  
 TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAATGCG TGTTACGTGA 120  
 25 TCATGATACT GTCAn 135

## (2) INFORMATION FOR SEQ ID NO: 4742:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

35 ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60  
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120  
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

## (2) INFORMATION FOR SEQ ID NO: 4743:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120

TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

5 (2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60

AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120

20 TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 25 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAAC 60

35 TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120

AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60

50 GATTCAGACA GCGATTTCAGA TTCAGATAGC GATTTCAGATT CCGACAGTGA CTCAGATTCC 120

GACAnTGACT CGGATTCA 138

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAAC TTTCGTCACTT GCTGGTGTGTT GGGGACCCCA CCAACTTGGC 60  
 ACATTATTGG TAAGCTGACT TTTCGTCACT TACTGTGTG GGGCCCCGCC AACTTGCATT 120  
 GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180  
 GCCTG 185

## (2) INFORMATION FOR SEQ ID NO: 4748:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60  
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120  
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

## (2) INFORMATION FOR SEQ ID NO: 4749:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60  
 CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120  
 AATTAAAGGG CATGCAACCA AGTANCTGAG GAAACAACTT ATTTTCATGG TGTCAAAAAT 180  
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

## (2) INFORMATION FOR SEQ ID NO: 4750:

(A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAGAGT TTTAAATAAG CTTGAATTCA 60  
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTTAAATCTT 120  
 TTTATAAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60  
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120  
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180  
 TCCG 184

35

(2) INFORMATION FOR SEQ ID NO: 4752:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AAAGTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60  
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120  
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCA TGTTGGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60  
 ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120  
 TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG 162

## (2) INFORMATION FOR SEQ ID NO: 4754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTG CCTTAGTAGC GGCGACGAAA ACGGGAANGA GCCCAAACCA ACAAGCTTGC 60  
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120  
 CTTGGGAAAG ATGA 134

## (2) INFORMATION FOR SEQ ID NO: 4755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCCTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60  
 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120  
 40 TGAAGCATGn ATCGTAAGG 139

## (2) INFORMATION FOR SEQ ID NO: 4756:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:



CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120  
 ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 60  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAGAT 120  
 TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60  
 GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120  
 ACTGCTGTTC TCTATTTATA CCAATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60  
 ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG 120  
 ATTGCT 127

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCCTCG TCGGGTTACC GAATTCAGAC AAACCTCCGnA ATGCCAATTA ATTTAACTTG 60  
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120  
 AGTCCCAAAT ATATGTTAAT GAAAG 145

15

## (2) INFORMATION FOR SEQ ID NO: 4761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60  
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120  
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180  
 TTAACACACC AAAACAGCTC CCACCACCAC TAAATCGAnC AACACTAG 228

30

35

## (2) INFORMATION FOR SEQ ID NO: 4762:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60  
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC 120  
 AGCAGGGTTG 130

50

## (2) INFORMATION FOR SEQ ID NO: 4763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60  
10 GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120  
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60  
25 CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120  
TACTGCCA 128

30 (2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

40

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60  
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120  
45 TTTCCATGTG GnaAC 135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
50 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60  
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCTTA CCATTGTCCA AAGGACAATC 120  
 CACAGC 126

## (2) INFORMATION FOR SEQ ID NO: 4767:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60  
 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120  
 GATTTTTTAAC 130

## (2) INFORMATION FOR SEQ ID NO: 4768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60  
 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120  
 TAGGGCACCT ATTTTCCTAT CT 142

## (2) INFORMATION FOR SEQ ID NO: 4769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60  
 CGTCGATGTG AACTCTTnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60  
 ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120  
 TAGAGCTATT AAGCGTnGCC ATGAG 145

## (2) INFORMATION FOR SEQ ID NO: 4771:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60  
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120  
 ATGTGGGA 128

## (2) INFORMATION FOR SEQ ID NO: 4772:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA 60  
 ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTTGGTGT 120  
 GTACTT 126

## (2) INFORMATION FOR SEQ ID NO: 4773:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCCTTTCTC GTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60  
10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAn ACCTTGCGGT CTCAATGCGG 120  
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60  
TGCATCTTnA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120  
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60  
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAncCAGAA ACTCCAACAC CGCCAACACC 120  
45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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55

CCCGCTAGTC TCCACCATTT ATTTTTTACA CGATGAACAT TGAAACTnA ATACAATATG 60  
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120  
 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60  
 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC TGACGCTGGAT GTGCGAAACG 120  
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60  
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCACTGCTC 120  
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAACTATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60  
 AACAAATATAG CTCAGGTATT ACGTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60  
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120  
 TCCTTTT 127

## (2) INFORMATION FOR SEQ ID NO: 4781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60  
 GTCTTATTTT TTAAAGTAT TAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120  
 CGAGACTCC 129

## (2) INFORMATION FOR SEQ ID NO: 4782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCTCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60  
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG 120  
 GTCAGATTTA GGACCA 136

## (2) INFORMATION FOR SEQ ID NO: 4783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60  
10 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60  
25 nATCCCATTTG CATCCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120  
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60  
40 ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

(i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCAACCAC TTTATCGTGG TGGGGAGACA GTGTTcAGGC GGGCCAGTTT 60  
55

AATCATTCAT AGAGTGT

137

## (2) INFORMATION FOR SEQ ID NO: 4787:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

15

GTTTTTAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AaATACCTTT 60

TTCATCTTGG TCTTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

## (2) INFORMATION FOR SEQ ID NO: 4788:

20

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

30

CATGCTTCCA CCTCGAACCT ATTAACCTnc ATCATCTTTG AGGGATCTTA TAACCGCAGT 60

TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120

GCCACACATA GCTACCCAGC T 141

## (2) INFORMATION FOR SEQ ID NO: 4789:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

45

CTGGGTTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60

AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120

50

GCCAACGCAT AGCTGGGTA 139

## (2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AncATAATTT TTATGGAGAG TTTGATCCTG 60  
10 GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120  
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60  
25 TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTAC GCCTGAAATG GCTTCTTGCC 60  
40 AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120  
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

55

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120  
 nCCTGATAAC 130

5 (2) INFORMATION FOR SEQ ID NO: 4794:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60  
 TAACTCATT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

20 (2) INFORMATION FOR SEQ ID NO: 4795:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCCAATT TTTTTTGGGG GGTGGGAAT TTAAAAATTT GGTTTTTAAC 60  
 CCAAAGGCC TTTTCCCAA AATTAAATT CCCTTAAAAA TTAAAAATTT GGGAATTTTT 120  
 35 TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCA ATTTTAAATT TAACCCTTAA 180  
 AACCCCAAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

(2) INFORMATION FOR SEQ ID NO: 4796:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

50 TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60  
 GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACTCTT GGGGGCAGAT 120

55 (2) INFORMATION FOR SEQ ID NO: 4797:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTG CCTTAGTAGC GCGGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60  
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120  
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60  
 AACCCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 116 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60  
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

TCAGTGCAT GATTTCGTGAA ATTGAAACGC AAGATTTCTGA TATCGAnCAC CT

112

(2) INFORMATION FOR SEQ ID NO: 4801:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA

60

ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC

110

(2) INFORMATION FOR SEQ ID NO: 4802:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT

60

TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAAATT AACGTCTTCT GCAGTCGCAC

120

CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA

180

CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA

237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC

60

AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG

114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60  
10 GTTAGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60  
25 CCAGGAAAGT CGCCTTCGCC ACTGGTGTTT CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60  
40 GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60  
55 TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

## (2) INFORMATION FOR SEQ ID NO: 4808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60  
 ATCATTGCTA GCTTTTCTTG TATTAAGTGA TANTTACTAA TTGGTTTGCC GAATTGCT 118

## (2) INFORMATION FOR SEQ ID NO: 4809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCTGA TTGGAATTTTC 60  
 TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120  
 TACCTGACTT CAACTGACCA GGGTAGACAC 150

## (2) INFORMATION FOR SEQ ID NO: 4810:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCCA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCan 60  
 AAACGTAAAT TCATGTTGGT GATAAGATGT GTGCTCGACA TGGTACA 107

## (2) INFORMATION FOR SEQ ID NO: 4811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTTCG AGGAAGACAC 60  
5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60  
20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120  
ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60  
35 TAGCCCTAAA GCTATTTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60  
50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

- (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GGCGGCGGTT GAACCCGTCA TTCTGCACCA 60  
 TTTATTCTTA CATATTGCCG G<sub>n</sub>CTAGCTCA ATTGGTAGAG CAACTGACCT TGTAAATCAGT 120  
 AGGTT 125

15

(2) INFORMATION FOR SEQ ID NO: 4816:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

25

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60  
 CTGTTGCTTA CACTGAAGAC GTTTATG<sub>n</sub>TT TCTGGCGTCC AACT 104

30

(2) INFORMATION FOR SEQ ID NO: 4817:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40

GTCGGGTAAG TTCCGGCCCC CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACG<sub>n</sub>GAG 60  
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45

(2) INFORMATION FOR SEQ ID NO: 4818:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

55

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120

A 121

5 (2) INFORMATION FOR SEQ ID NO: 4819:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

20 (2) INFORMATION FOR SEQ ID NO: 4820:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

35 (2) INFORMATION FOR SEQ ID NO: 4821:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

45 TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

50 (2) INFORMATION FOR SEQ ID NO: 4822:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs

55

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

25 TTTGANTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCTTGTGTC GGGTAAGTTC 60

40 CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA ACTAGAGn 108

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

55 nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60  
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120  
 ATCCTTGTAT TCGGTGTCAT AaAGTCTTTG CTCCTTGAC 160

## (2) INFORMATION FOR SEQ ID NO: 4827:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60  
 AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

## (2) INFORMATION FOR SEQ ID NO: 4828:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60  
 TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

## (2) INFORMATION FOR SEQ ID NO: 4829:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCAGGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60  
 GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60  
 TTTCGTTTCTAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60  
 AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TnTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60  
 TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60  
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120  
 TTTTCAGCAT CAATTGATC AATC 144

## (2) INFORMATION FOR SEQ ID NO: 4834:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60  
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

## (2) INFORMATION FOR SEQ ID NO: 4835:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GgGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60  
 CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

## (2) INFORMATION FOR SEQ ID NO: 4836:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG 60  
 TTTGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60  
 CGGAATTTCa ATTTCaGc TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60  
 GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120  
 A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60  
 ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60  
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTGGGCTTT 120  
 CTAACCC 127

## (2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTIONAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60  
 CATTCACTCA ACTACTGCCA ATATAATATT GnaAACTATA GGACATTTAT TAGTGTTC 120  
 GTTCT 125

## (2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60  
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

## (2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTGGGATCG TAAAACTCTG TTATTAAGna GGAACATGTG TGTAAGTAGC 60  
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

## (2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60  
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

GACTGTTTAT CAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60  
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60  
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60  
 CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120  
 CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA CTTACCG 60  
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60  
 TTATAGTTAC GGTCCGCCGT TTA CTTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120  
 CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 96 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TAAAAATAG TTCTTTAAAT TATATACCCA CCACATTGG TGGGAGAACC 60  
TAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

## (2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTCCT TTTGTAGnAT 60  
GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

## (2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

30 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTA 60  
35 ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

## (2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

45 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60  
50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

## (2) INFORMATION FOR SEQ ID NO: 4855:

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- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60  
 CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

25 CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60  
 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120  
 CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60  
 TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCCTG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAAC TCGCC GGTT CATTCT ACAA AAGGCG ACGCCAATCA CCCATTAACG GGCTCCTGAA 60  
 CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTCCA CTTCCCCTTT CCGGGGTnGC 120  
 TTTTTC AACC TTTTCCCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60  
 CTCTCGTTAA GGAAC TCGGC AAAC TGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60  
 AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

## (2) INFORMATION FOR SEQ ID NO: 4863:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

## (2) INFORMATION FOR SEQ ID NO: 4864:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60  
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120  
 GCAnTGGCT 129

## (2) INFORMATION FOR SEQ ID NO: 4865:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60  
 TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60  
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60  
CGGTTTAGCA GAGACCTGTG TTTTGTATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCCT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60  
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 165 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:



CGCTCACCTT AGAATCTATT TACACTGGTG TTGGTAGGCA CTTTTTTC AA GCTTCCGATT 120  
AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

5 (2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 111 base pairs  
    (B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTAAACC 60  
AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

20 (2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 84 base pairs  
    (B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCAC TG CGGCTCTTCT 60  
GGGCGTTAAC CCTAAAGAGC ACCC 84

35 (2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 101 base pairs  
    (B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60  
ATGATTTTAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C 101

50 (2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 87 base pairs  
    (B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GCGGATGGAT AACAGGTTGT ATTCTGTAC CACCTATGAT CGTTTTAATC 60  
GATGGGGGGA AGCATAGGAT AGGCGAA 87

## (2) INFORMATION FOR SEQ ID NO: 4874:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTG ATCCCGCTAG TCTCCACCAT 60  
TATTTGTACA TTGAAACTA G 81

## (2) INFORMATION FOR SEQ ID NO: 4875:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

30 TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60  
35 CGAACTGAAT AAATAAGAT T 81

## (2) INFORMATION FOR SEQ ID NO: 4876:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

45 AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60  
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

## (2) INFORMATION FOR SEQ ID NO: 4877:

55

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60  
 CGGGGAGGTT TGCCTCAAT GTGGCTCATC GGATCTTGGG G 101

## (2) INFORMATION FOR SEQ ID NO: 4878:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60  
 CAACTGCATG AGGTATATT 79

## (2) INFORMATION FOR SEQ ID NO: 4879:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60  
 AAATTGGTAT GGTAATTGTG GCA 83

## (2) INFORMATION FOR SEQ ID NO: 4880:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

## (2) INFORMATION FOR SEQ ID NO: 4881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60  
 CTTCACGCTT CTTGCGCATT 80

## (2) INFORMATION FOR SEQ ID NO: 4882:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCACGG CTCAACCGTG GAGGGTCATT GGAACTGGA AAAGTTGAGT 60  
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

## (2) INFORMATION FOR SEQ ID NO: 4883:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60  
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120  
 CGGTTAA 127

## (2) INFORMATION FOR SEQ ID NO: 4884:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60  
 CTATTAAAAA TAATAAAT 78

## (2) INFORMATION FOR SEQ ID NO: 4885:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGG CTAAACATAT TACCGAAGCT 60  
 GTGGATTGTC CTTTGAAAT GGGT 84

## (2) INFORMATION FOR SEQ ID NO: 4886:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCCG GTGGTGCAGT TGCGACCAAC AATGGGTTGG AGATTGGATT 60  
 TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAATGG TACCCCATCC AAAAGGG 117

## (2) INFORMATION FOR SEQ ID NO: 4887:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60  
 ACCGTGAGGA AAGGTGAAAA 80

## (2) INFORMATION FOR SEQ ID NO: 4888:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGGCCGA 60

GTTCCTTAAC GAGAGT 76

25

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGGCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCAIT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 88 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60  
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG GCAGTTCGAA 60  
TCTGCCCCC TCCATTTATT ATTTTAAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTG CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60  
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 141 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120  
TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 80 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTCGGATTT AATTGATTC ATTTGTTGCG TAATTTTCTA AGCCATTTTA TGAAAAGAGT 60  
GATTTAATTC ATAAATTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 73 base pairs  
    (B) TYPE: nucleic acid  
25     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60  
AAACCAATTA GTA 73

35 (2) INFORMATION FOR SEQ ID NO: 4898:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 71 base pairs  
    (B) TYPE: nucleic acid  
40     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60  
TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- 50 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 116 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60  
 TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGGC TGGTTT 116

## (2) INFORMATION FOR SEQ ID NO: 4900:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGThTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60  
 CGGGCAGAGT CCCCTTCGAC TAAGAAATC TCACATTCTT CAGGGACTTT TAC 113

## (2) INFORMATION FOR SEQ ID NO: 4901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60  
 AAAAATAGGG AATACATG 78

## (2) INFORMATION FOR SEQ ID NO: 4902:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60  
 CAAAACTAGA TAGTAAGTAA AAGT 84

## (2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60  
 AGACTCGGTG 70

## (2) INFORMATION FOR SEQ ID NO: 4904:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120  
 GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

## (2) INFORMATION FOR SEQ ID NO: 4905:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60  
 TTATCGTGGT GGGGA 75

## (2) INFORMATION FOR SEQ ID NO: 4906:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGA CTCAGAT CAGATAGTgn CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 70 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

15

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA

60

AGGTTTACCA

70

(2) INFORMATION FOR SEQ ID NO: 4908:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

30

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTC GGTGGGACAC AATAGTGTG

60

ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC

120

C

121

35

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 70 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

45

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCTGA GATGTTGGGG

60

TTAAGTCCCG

70

50

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCGG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60

TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60

20 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTTGAT 120

GTAACTTTG GCACATCAGC TTTTAGTGTG TTTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

35 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60

AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

50 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA 60

GCGGAACGT 69

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60  
 ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60  
 CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTCTT ATTTCACTCC 60  
 CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120  
GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

5 (2) INFORMATION FOR SEQ ID NO: 4918:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60  
ACATATGT 68

20 (2) INFORMATION FOR SEQ ID NO: 4919:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 base pairs  
    (B) TYPE: nucleic acid  
25     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60  
AGTGACAATA CTTCAGGG 78

35 (2) INFORMATION FOR SEQ ID NO: 4920:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
40     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCGTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTGATTTCG 60  
TACTTCGC 68

50 (2) INFORMATION FOR SEQ ID NO: 4921:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 67 base pairs  
    (B) TYPE: nucleic acid  
55     (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60  
TTTACTG 67

## (2) INFORMATION FOR SEQ ID NO: 4922:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

20 GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60  
GTCATG 66

## (2) INFORMATION FOR SEQ ID NO: 4923:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

30 GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60  
35 TCGTGGGTGG GAG 73

## (2) INFORMATION FOR SEQ ID NO: 4924:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

45 GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60  
50 TGATGACATA TGCACCGTAA TTCCAAAAA 89

## (2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60  
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTTG GGCACGTATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60  
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

ATTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60  
40 CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

55



## (2) INFORMATION FOR SEQ ID NO: 4929:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60  
GTGGGTCCCG ACACAGAGAA ATT 83

## (2) INFORMATION FOR SEQ ID NO: 4930:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60  
ACTCTA 66

## (2) INFORMATION FOR SEQ ID NO: 4931:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60  
GACCG 65

## (2) INFORMATION FOR SEQ ID NO: 4932:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60  
CACCAGTGGG CGA 73

5 (2) INFORMATION FOR SEQ ID NO: 4933:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60  
GTCTG 65

20 (2) INFORMATION FOR SEQ ID NO: 4934:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60  
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTCGGGGT AACAAATGTA CAGGTTGGTG 120

35 (2) INFORMATION FOR SEQ ID NO: 4935:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60  
GGATAACGGT TG 72

50 (2) INFORMATION FOR SEQ ID NO: 4936:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTT CTCCATATCT 60  
CTGC 64

## (2) INFORMATION FOR SEQ ID NO: 4937:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60  
20 TGGT 64

## (2) INFORMATION FOR SEQ ID NO: 4938:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

30 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60  
35 GAT 63

## (2) INFORMATION FOR SEQ ID NO: 4939:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

45 TAGAAATCAG CTTTTTTGCA TAGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60  
CCT 63

## (2) INFORMATION FOR SEQ ID NO: 4940:

- (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60  
 TAGCTCAG 68

## (2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60  
 CG 62

## (2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60  
 TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

## (2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AACATTATT 60

55

## (2) INFORMATION FOR SEQ ID NO: 4944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60  
 GACGAATACG TAATTGA 77

## (2) INFORMATION FOR SEQ ID NO: 4945:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60  
 CAGGTAACAC TGAAT 75

## (2) INFORMATION FOR SEQ ID NO: 4946:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60  
 TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120  
 TACAGCGCTG AACT 135

## (2) INFORMATION FOR SEQ ID NO: 4947:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

5 GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTCC 60  
T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

20 GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60  
TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

35 CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60  
CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

50 GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60  
TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

50

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT

59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

20

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC

59

(2) INFORMATION FOR SEQ ID NO: 4957:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAATCTAT ATTTTACTTA CTTATCTAGT

60

35

TTTCAATGTA CAATTTC

77

(2) INFORMATION FOR SEQ ID NO: 4958:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCTGT AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCTTAA

59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG

59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAC TGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA

59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA

59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA

59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG

60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG

59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTAGC

59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG

59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTGGCGCT ATGTATATCG CATTAAACGT

60

## (2) INFORMATION FOR SEQ ID NO: 4968:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTITAGAGG CGACGCCAG TCAAAGTCC CGCTGACACT GTCTCCCACC 60

## (2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

## (2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60  
TTACG 65

## (2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGAATTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60  
 AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATCATGC ATAAGAAATA CTAATTTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTTCA CCCTGACTCG ACTTGTAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

25

AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60  
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

35 TGATGAAGGT CTCGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

55

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA

57

10

(2) INFORMATION FOR SEQ ID NO: 4989:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

20

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG

57

(2) INFORMATION FOR SEQ ID NO: 4990:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT

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G

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(2) INFORMATION FOR SEQ ID NO: 4991:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC

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ACCGA

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(2) INFORMATION FOR SEQ ID NO: 4992:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT

57

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(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

CCAATGCGGC TCATCGCATC CATTITTTTGC CTGGCAACGT TCTACTCTAG CGGAACG

57

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(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGITTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG

57

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(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

CAAACCTCTCG TGGTGTGACG GCGGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC

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ATGCCGGTCT ACG

73

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(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG  
TAAGC

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(2) INFORMATION FOR SEQ ID NO: 4997:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT

58

(2) INFORMATION FOR SEQ ID NO: 4998:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GTTTTTCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG

56

(2) INFORMATION FOR SEQ ID NO: 4999:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT

56

(2) INFORMATION FOR SEQ ID NO: 5000:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTGCGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATT AGCTCTACTA AACTCGTTC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

## (2) INFORMATION FOR SEQ ID NO: 5005:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCCTAGAA GCCGATG

## (2) INFORMATION FOR SEQ ID NO: 5006:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCAC TCCCCTG

## (2) INFORMATION FOR SEQ ID NO: 5007:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA  
AACCAAAGA

## (2) INFORMATION FOR SEQ ID NO: 5008:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

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ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

56

- (2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC

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TTGGG

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- (2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

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- (2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGATAA ACAGTCGCTT

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- (2) INFORMATION FOR SEQ ID NO: 5013:

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- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAA TTGTGCAAGT TGGCGGGTCC 60  
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCACT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 105 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60  
40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

(2) INFORMATION FOR SEQ ID NO: 5017:

55

- (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60  
TATTG 65

## (2) INFORMATION FOR SEQ ID NO: 5018:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

## (2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

35 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

40

## (2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

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TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

## (2) INFORMATION FOR SEQ ID NO: 5021:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA

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10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

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AGAGTTCACA TCGACGGGGA GGTTCGGCAC CTCGATGTCG GTCATCGCA TCCTG

55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC

58

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(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT

55

(2) INFORMATION FOR SEQ ID NO: 5025:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGAATT 60

5 CCA 63

## (2) INFORMATION FOR SEQ ID NO: 5026:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60

20 AACG 64

## (2) INFORMATION FOR SEQ ID NO: 5027:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

## 35 (2) INFORMATION FOR SEQ ID NO: 5028:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

## (2) INFORMATION FOR SEQ ID NO: 5029:

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 57 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGACTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAACCTCTG TGTTCCGGCAT GGGAACAGGT GTGA

54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG

56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCAACGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

(2) INFORMATION FOR SEQ ID NO: 5040:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35 TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

(2) INFORMATION FOR SEQ ID NO: 5041:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50 GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

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(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

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(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

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TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

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(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

5 CGTCATCCCC ACCTTCCTCC GGTTCGTCAC CGGCAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

30 CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA 53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT 59

45 (2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60  
TTACGTTGAC TTAAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
25     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

30 CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 base pairs  
35     (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
50     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

55

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTCTTTT GCATAATTGA  
 CAA

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG



- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA 59

(2) INFORMATION FOR SEQ ID NO: 5060:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT 53

25

(2) INFORMATION FOR SEQ ID NO: 5061:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC 55

(2) INFORMATION FOR SEQ ID NO: 5062:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTTCGC ACATCAGCGT CA 52

50

(2) INFORMATION FOR SEQ ID NO: 5063:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTGAC GTTTTAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTC GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

CCACCGCTTG TCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCTT TTGG

74

## (2) INFORMATION FOR SEQ ID NO: 5076:

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

15

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

## (2) INFORMATION FOR SEQ ID NO: 5077:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA

52

## (2) INFORMATION FOR SEQ ID NO: 5078:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

40

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA AC

52

## (2) INFORMATION FOR SEQ ID NO: 5079:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

55

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG 52

(2) INFORMATION FOR SEQ ID NO: 5081:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA 52

25

(2) INFORMATION FOR SEQ ID NO: 5082:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA 56

(2) INFORMATION FOR SEQ ID NO: 5083:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

50 AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA 60

CG 62

(2) INFORMATION FOR SEQ ID NO: 5084:

55

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10 GTGTACCACT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC 60

CCGAGGAGCG GATTAACA 78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50 AAGTTGTTCT CAGTTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T

51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCGGTC C

51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

15 GGGTCTGTTT TCTAATTGA GCACAATCTT CGTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

40 CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60  
 CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10

ATTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTTGA

50

(2) INFORMATION FOR SEQ ID NO: 5107:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA

50

(2) INFORMATION FOR SEQ ID NO: 5109:

50

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAACT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTGGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAACTCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

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(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

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CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

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- (2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

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- (2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

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- (2) INFORMATION FOR SEQ ID NO: 5121:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

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61

- (2) INFORMATION FOR SEQ ID NO: 5122:

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- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTCAGA CAGCGACTCA GACTCAGATA. 50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT 50

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35 CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT 60

50

AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

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GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG

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(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTITA GCAGTTGTTG CTCGTTCAA TTTTATGGGG CCATTTATGG

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35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

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TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTGAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

## (2) INFORMATION FOR SEQ ID NO: 5135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

## (2) INFORMATION FOR SEQ ID NO: 5136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

## (2) INFORMATION FOR SEQ ID NO: 5137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

## (2) INFORMATION FOR SEQ ID NO: 5138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

## (2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC

52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT

56

25 (2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35 AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT

56

50 (2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT  
CGCCATTGCG AAGAT

60  
75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT

55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG

53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T

51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GAAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACCT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAACCTT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

15

(2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

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TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

30

(2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

40

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

45

(2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

55

(2) INFORMATION FOR SEQ ID NO: 5156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

(2) INFORMATION FOR SEQ ID NO: 5157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G 51

(2) INFORMATION FOR SEQ ID NO: 5158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

(2) INFORMATION FOR SEQ ID NO: 5159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

(2) INFORMATION FOR SEQ ID NO: 5160:



(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCTTTGTAT 60  
T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

35 CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50 CTTGATCTGT ATTAAATG ATATTTTCTA TCTTTTCTTT ATTATTAAACG TCTATGACGT 60  
CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

55

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60  
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAC TG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60  
40 AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

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- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATAAGTAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA

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(2) INFORMATION FOR SEQ ID NO: 5170:

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAGCT GATTCTATT

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(2) INFORMATION FOR SEQ ID NO: 5172:

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATG CCATTGGAAG

60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn

50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAAATAC CCCGTAACCT CGGAGTAGGT CTCITTTA

57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA

60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

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AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

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(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCGGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 83 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

40

CGGTAACCTC ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

55

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

15 GTTCGGTAAC TCGAGCGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC  
GCAATAT

60

67

(2) INFORMATION FOR SEQ ID NO: 5182:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

30 TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCACTAG CGAAGGCAAC TTTCT

55

(2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

40 GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

50

(2) INFORMATION FOR SEQ ID NO: 5184:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

55

CC

62

## (2) INFORMATION FOR SEQ ID NO: 5185:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

15 GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

55

## (2) INFORMATION FOR SEQ ID NO: 5186:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

25 CCATCATTAAGTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

50

## (2) INFORMATION FOR SEQ ID NO: 5187:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

40 TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

50

## (2) INFORMATION FOR SEQ ID NO: 5188:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

55 AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

10

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

54

(2) INFORMATION FOR SEQ ID NO: 5190:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

25

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

50

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

35

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

60

(2) INFORMATION FOR SEQ ID NO: 5192:

40

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu  
 1 5 10 15

55



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	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
40	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
45	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu  
 1 5 10 15  
 Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn  
 20 25 30  
 Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu  
 35 40 45  
 Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr  
 50 55 60  
 Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser  
 65 70 75 80  
 Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp  
 85 90 95  
 Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser  
 100 105 110  
 Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys  
 115 120 125  
 Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr  
 130 135 140  
 Val Phe Lys Phe Lys Asp Thr Thr Lys Leu Met Gly Lys Ala Leu Gly  
 145 150 155 160  
 Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val  
 165 170 175  
 Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro  
 180 185 190  
 Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr  
 195 200 205  
 Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg  
 210 215 220  
 Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln  
 225 230 235 240  
 Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe  
 245 250 255

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Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys  
260 265 270

Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala  
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn  
290 295 300

Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr  
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys  
325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile  
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly  
20 25 30

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr  
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe  
50 55 60

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val  
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val  
85 90 95

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala  
100 105 110

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly  
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile  
130 135 140

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn  
145 150 155 160

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Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn  
165 170 175

Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala  
180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr  
195 200 205

Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu  
210 215 220

Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp  
225 230 235 240

Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu  
245 250 255

Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val  
260 265 270

Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly  
275 280 285

Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn  
290 295 300

Lys Asn Leu Arg Leu Xaa Ser His Lys Gln  
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala  
1 5 10 15

Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser  
20 25 30

Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp  
35 40 45

Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn  
50 55 60

Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe  
65 70 75 80

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Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser  
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys  
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro  
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala  
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys  
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala  
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn  
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile  
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile  
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile  
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp  
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys  
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys  
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val  
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys  
20 25 30

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Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys  
35 40 45

5 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr  
50 55 60

Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile  
65 70 75 80

10 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys  
85 90 95

Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro  
100 105 110

15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys  
115 120 125

Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe  
130 135 140

20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val  
145 150 155 160

Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp  
165 170 175

25 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr  
180 185 190

Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile  
195 200 205

Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala  
210 215 220

35 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln  
225 230 235 240

Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp  
245 250 255

40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala  
260 265 270

Lys

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
35	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys  
305 310

## (2) INFORMATION FOR SEQ ID NO:5198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15  
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30  
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
25 35 40 45  
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60  
Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
30 65 70 75 80  
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95  
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
35 100 105 110  
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125  
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
40 130 135 140  
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
45 145 150 155 160  
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175  
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
50 180 185 190  
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
195 200 205  
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
55 210 215 220



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Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175

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Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
180 185 190  
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
195 200 205  
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
210 215 220  
Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
225 230 235 240  
Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
245 250 255  
Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
260 265 270  
Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
275 280

(2) INFORMATION FOR SEQ ID NO:5200:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 208 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu  
1 5 10 15  
Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn  
20 25 30  
Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn  
35 40 45  
Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn  
50 55 60  
Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys  
65 70 75 80  
Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu  
85 90 95  
Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn  
100 105 110  
Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys  
115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn  
130 135 140

5 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile  
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro  
165 170 175

10 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu  
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys  
195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

30 Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile  
1 5 10 15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser  
20 25 30

35 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn  
35 40 45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu  
50 55 60

40 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn  
65 70 75 80

45 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp  
85 90 95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu  
100 105 110

50 Lys Asp Asp Leu Lys Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser  
115 120 125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser  
130 135 140

55 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys  
 165 170 175

5 Arg Ala Cys Glu Pro Asp Lys Tyr  
 180

(2) INFORMATION FOR SEQ ID NO:5202:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile  
 1 5 10 15  
 Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr  
 25 20 25 30  
 Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys  
 35 40 45  
 Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu  
 50 55 60  
 Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu  
 65 70 75 80  
 Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser  
 85 90 95  
 Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser  
 100 105 110  
 Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu  
 115 120 125  
 Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn  
 130 135 140  
 Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile  
 145 150 155 160  
 Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val  
 50 165 170 175  
 Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile  
 180 185 190  
 Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys  
 55

## (2) INFORMATION FOR SEQ ID NO:5203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser  
 1                      5                      10                      15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr  
                     20                      25                      30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu  
                     35                      40                      45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr  
                     50                      55                      60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly  
                     65                      70                      75                      80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu  
                     85                      90                      95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp  
                     100                      105                      110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr  
                     115                      120                      125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly  
                     130                      135                      140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser  
                     145                      150                      155                      160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr  
                     165                      170                      175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala  
                     180                      185                      190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly  
                     195                      200                      205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys  
                     210                      215                      220

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	225		230		235		240
	Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro						
5		245		250		255	
	Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln						
		260		265		270	
10	Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile						
	275		280				

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

25	Met	Lys	Lys	Phe	Ile	Gly	Ser	Val	Leu	Ala	Thr	Thr	Leu	Ile	Leu	Gly
	1				5					10					15	
	Gly	Cys	Ser	Thr	Met	Glu	Asn	Glu	Ser	Lys	Lys	Asp	Thr	Lys	Thr	Glu
30				20					25					30		
	Thr	Lys	Ser	Val	Pro	Glu	Glu	Met	Glu	Ala	Ser	Lys	Tyr	Val	Gly	Gln
			35					40					45			
	Gly	Phe	Gln	Pro	Pro	Ala	Glu	Lys	Asn	Ala	Ile	Glu	Phe	Ala	Lys	Lys
35		50					55					60				
	His	Arg	Lys	Glu	Phe	Glu	Lys	Val	Gly	Glu	Gln	Phe	Phe	Lys	Asp	Asn
	65					70					75					80
	Phe	Gly	Leu	Lys	Val	Lys	Ala	Thr	Asn	Val	Val	Gly	Lys	Asp	Asp	Gly
40					85					90					95	
	Val	Glu	Val	Tyr	Val	His	Cys	Glu	Asp	His	Gly	Ile	Val	Phe	Asn	Ala
				100					105					110		
	Ser	Leu	Pro	Leu	Tyr	Lys	Asp	Ala	Ile	His	Gln	Lys	Gly	Ser	Met	Arg
45			115					120					125			
	Ser	Asn	Asp	Asn	Gly	Asp	Asp	Met	Ser	Met	Met	Val	Gly	Thr	Val	Leu
		130					135					140				
	Ser	Gly	Phe	Glu	Tyr	Arg	Ala	Gln	Lys	Glu	Lys	Tyr	Asp	Asn	Leu	Tyr
50	145					150				155						160
	Lys	Phe	Phe	Lys	Glu	Asn	Glu	Lys	Lys	Tyr	Gln	Tyr	Thr	Gly	Phe	Thr
					165					170						175

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180 185 190

Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr  
195 200 205

Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met  
210 215 220

Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val  
225 230 235 240

Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val  
245 250 255

Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys  
260 265 270

Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn  
275 280 285

Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val  
290 295 300

His Ser Lys Asp Glu  
305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly  
1 5 10 15

Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu  
20 25 30

Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln  
35 40 45

Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys  
50 55 60

Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met  
65 70 75 80

Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser  
85 90 95

100 105 110  
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His  
 115 120 125  
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp  
 130 135 140  
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His  
 10 145 150 155 160  
 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln  
 165 170 175  
 15 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys  
 180 185 190  
 Ser

20 (2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 25 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

35 Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala  
 1 5 10 15  
 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser  
 20 25 30  
 40 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe  
 35 40 45  
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys  
 50 55 60  
 45 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser  
 65 70 75 80  
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile  
 85 90 95  
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe  
 100 105 110  
 55 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn  
 115 120 125



130                      135                      140  
 Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala  
 145                      150                      155                      160  
 5  
 Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu  
 165                      170                      175  
 Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp  
 180                      185                      190  
 10  
 Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn  
 195                      200                      205  
 Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp  
 210                      215                      220  
 15  
 Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn  
 225                      230                      235                      240  
 20  
 Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser  
 245                      250                      255  
 Lys Ser Lys

25 (2) INFORMATION FOR SEQ ID NO:5207:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 amino acids  
 (B) TYPE: amino acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile  
 1                      5                      10                      15  
 40  
 Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn  
 20                      25                      30  
 45  
 Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln  
 35                      40                      45  
 Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser  
 50                      55                      60  
 50  
 Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly  
 65                      70                      75                      80  
 Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp  
 85                      90                      95  
 55

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100 105 110

Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu  
115 120 125

Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp  
130 135 140

Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys  
145 150 155 160

Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu  
165 170 175

Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val  
180 185 190

Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr  
195 200

(2) INFORMATION FOR SEQ ID NO:5208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu  
1 5 10 15

Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp  
20 25 30

Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile  
35 40 45

Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys  
50 55 60

Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile  
65 70 75 80

Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu  
85 90 95

Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys  
100 105 110

Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe  
115 120 125



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	35	40	45
5	Asn Leu Met Met Thr Lys 50	Lys Leu Leu Ser 55	Gln Tyr Asn His Pro Lys 60
	Tyr Lys Leu Glu Leu Val 65	Lys Phe Asn Asn Trp 70	Pro Asp Leu Met Asp 80
10	Ala Leu Asn Ser Gly Arg Ile 85	Asp Gly Ala Ser Thr 90	Leu Ile Glu Leu 95
	Ala Met Lys Ser Lys Gln Lys 100	Gly Ser Asn Ile Lys 105	Ala Val Ala Leu 110
15	Gly His His Glu Gly Asn Val 115	Ile Met Gly Gln Lys 120	Gly Met His Leu 125
	Asn Glu Phe Asn Asn Asn 130	Gly Asp Asp Tyr His 135	Phe Gly Ile Pro His 140
20	Arg Tyr Ser Thr His Tyr 145	Leu Leu Leu Glu Glu 150	Leu Arg Lys Gln Leu 155
	Lys Ile Lys Pro Gly His Phe 165	Ser Tyr His Glu Met 170	Ser Pro Ala Glu 175
25	Met Pro Ala Ala Leu Ser 180	Glu His Arg Ile Thr 185	Gly Tyr Ser Val Ala 190
	Glu Pro Phe Gly Ala Leu 195	Gly Glu Lys Leu Gly 200	Lys Gly Lys Thr Leu 205
30	Lys His Gly Asp Asp Val 210	Ile Pro Asp Ala Tyr 215	Cys Cys Val Leu Val 220
	Leu Arg Gly Glu Leu Leu 225	Asp Gln His Lys Asp 230	Val Ala Gln Ala Phe 235
35	Val Gln Asp Tyr Lys Lys 245	Ser Gly Phe Lys Met 250	Asn Asp Arg Lys Gln 255
	Ser Val Asp Ile Met Thr 260	His His Phe Lys Gln 265	Ser Arg Asp Val Leu 270
40	Thr Gln Ser Ala Ala Trp 275	Thr Ser Tyr Gly Asp 280	Leu Thr Ile Lys Pro 285
	Ser Gly Tyr Gln Glu Ile 290	Thr Thr Leu Val Lys 295	Gln His His Leu Phe 300
45	Asn Pro Pro Ala Tyr Asp 305	Asp Phe Val Glu Pro 310	Ser Leu Tyr Lys Glu 315
50	Ala Ser Arg Ser		

(2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val  
 1 5 10 15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser  
 15 20 25 30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys  
 35 40 45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly  
 20 50 55 60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu  
 65 70 75 80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys  
 25 85 90 95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp  
 100 105 110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys  
 30 115 120 125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln  
 35 130 135 140

Val Asp Tyr Trp  
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp  
 1 5 10 15

55

20

25

30

His

5

## (2) INFORMATION FOR SEQ ID NO:5212:

## (i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 490 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys  
 1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn  
 20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly  
 35 40 45

30

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp  
 50 55 60

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn  
 65 70 75 80

35

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser  
 85 90 95

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr  
 100 105 110

40

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp  
 115 120 125

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg  
 130 135 140

45

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe  
 145 150 155 160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro  
 165 170 175

50

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile  
 180 185 190

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn  
 195 200 205

55

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	210	215	220
	Ala Glu Ala Tyr Arg	Asn Gly Leu Val	Asn Ala Pro Leu Ser Arg Leu
	225	230	235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val	Ser Gly Asn Thr Val	Trp Gln
	245	250	255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
10	260	265	270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
	275	280	285
15	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
	290	295	300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
	305	310	315 320
20	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
	325	330	335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
	340	345	350
25	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
	355	360	365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
	370	375	380
30	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
	385	390	395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
	405	410	415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
	420	425	430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
40	435	440	445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
	450	455	460
45	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
	465	470	475 480
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
	485	490	

(2) INFORMATION FOR SEQ ID NO:5213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu  
 1 5 10 15  
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala  
 20 25 30  
 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile  
 35 40 45  
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val  
 50 55 60  
 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly  
 65 70 75 80  
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys  
 85 90 95  
 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu  
 100 105 110  
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe  
 115 120 125  
 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val  
 130 135 140  
 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp  
 145 150 155 160  
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr  
 165 170 175  
 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His  
 180 185 190  
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln  
 195 200 205  
 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu  
 210 215 220  
 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala  
 225 230 235 240  
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe  
 245 250 255  
 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn  
 260 265 270



275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys  
 290 295

5

## (2) INFORMATION FOR SEQ ID NO:5214:

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

20

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn  
 1 5 10 15

Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr  
 20 25 30

25

Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro  
 35 40 45

Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn  
 50 55 60

30

Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro  
 65 70 75 80

Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp  
 85 90 95

35

Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala  
 100 105 110

Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln  
 115 120 125

40

Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg  
 130 135 140

45

Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys  
 145 150 155 160

Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu  
 165 170 175

50

Val Lys

## (2) INFORMATION FOR SEQ ID NO:5215:

55

## (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala  
 1 5 10 15  
 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala  
 20 25 30  
 Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp  
 35 40 45  
 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu  
 50 55 60  
 Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Asp Gly Thr Glu  
 65 70 75 80  
 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr  
 85 90 95  
 Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr  
 100 105 110  
 Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly  
 115 120 125  
 Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly  
 130 135 140  
 Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys  
 145 150 155 160  
 Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys  
 165 170

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

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1                      5                      10                      15  
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val  
                          20                                      25                                      30  
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile  
                          35                                      40                                      45  
 10 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn  
                          50                                      55                                      60  
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu  
 65                                      70                                      75                                      80  
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu  
    85                                      90                                      95  
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr  
    100                                      105                                      110  
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala  
    115                                      120                                      125  
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys  
 130                                      135                                      140  
 25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr  
 145                                      150                                      155                                      160  
 Asp Asp Asn Lys Gln Pro Ala  
 165  
 30

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 35

(ii) MOLECULE TYPE: protein  
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

45 Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser  
 1                                      5                                      10                                      15  
 Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys  
 20                                      25                                      30  
 50 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val  
                          35                                      40                                      45  
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val  
                          50                                      55                                      60

```

5      65      70      75      80
      Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
      85      90      95
      Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
      100      105      110
      Thr Ile Ser
      115
10

```

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

	Asn	Phe	Lys	Met	Gln	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys	
	1				5				10					15		
30	Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe
				20					25					30		
	Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu
			35					40					45			
35	Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile
		50					55					60				
	Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala
	65					70					75					80
40	Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe
					85					90					95	
	Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr
45				100					105					110		
	Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val
			115					120					125			
50	Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala
		130					135					140				
	Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe
	145					150					155					160
55	Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile			
					165					170						

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr  
 1 5 10 15  
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp  
 20 25 30  
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His  
 35 40 45  
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu  
 50 55 60  
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala  
 65 70 75 80  
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr  
 85 90 95  
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val  
 100 105 110  
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln  
 115 120 125  
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys  
 130 135

## (2) INFORMATION FOR SEQ ID NO:5220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val  
 1 5 10 15

[illegible]

(2) INFORMATION FOR SEQ ID NO:5221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

	Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu	
	1	5 10 15
45	Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn	
		20 25 30
50	Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu	
		35 40 45
	Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys	
		50 55 60
55	Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg	
		65 70 75 80

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	85	90	95
5	Asp Arg Arg Ile Glu Ile Asp Ile	Lys Ser Lys Asp Glu Ile Gly Asp	
	100	105	110
	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn		
	115	120	125
10	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His		
	130	135	140
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn		
	145	150	155
15	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr		
	165	170	175
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala		
	180	185	190
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn		
	195	200	205
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu		
	210	215	220
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile		
	225	230	235
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys		
	245	250	255
30	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp		
	260	265	270
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys		
	275	280	285
35	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys		
	290	295	300
40	Tyr Gln Asn Lys Leu Ala Ser		
	305	310	

(2) INFORMATION FOR SEQ ID NO:5222:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

[illegible]

(2) INFORMATION FOR SEQ ID NO:5223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser  
 1 5 10 15  
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg  
 20 25 30  
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu  
 35 40 45  
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn  
 50 55 60  
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe  
 65 70 75 80  
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr  
 85 90 95  
 Asp Leu Lys

## (2) INFORMATION FOR SEQ ID NO:5224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu  
 1 5 10 15  
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn  
 20 25 30  
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn  
 35 40 45  
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu  
 50 55 60  
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu  
 65 70 75 80  
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr  
 85 90 95  
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly  
 100 105 110

115

120

125

His Ser Ile  
130

## (2) INFORMATION FOR SEQ ID NO:5225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
1 5 10 15  
Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
20 25 30  
Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
35 40 45  
Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
50 55 60  
Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
65 70 75 80  
Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
85 90 95  
Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
100 105 110  
Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
115 120 125  
Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
130 135 140  
Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
145 150 155 160  
Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
165 170 175  
Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
180 185 190  
Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
195 200 205

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	210	215	220
5	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly 225 230 235 240		
	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn 245 250 255		
10	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val 260 265 270		
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys 275 280 285		
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr 290 295 300		
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp 305 310 315 320		
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly 325 330 335		
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu 340 345 350		
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr 355 360 365		
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly 370 375 380		
30	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro 385 390 395 400		
	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn 405 410 415		
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu 420 425 430		
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr 435 440 445		
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr 450 455 460		
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly 465 470 475 480		
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp 485 490 495		
50	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr 500 505 510		
	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser 515 520 525		

530

535

540

## (2) INFORMATION FOR SEQ ID NO:5226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His  
 1 5 10 15  
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val  
 20 25 30  
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile  
 35 40 45  
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His  
 50 55 60  
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe  
 65 70 75 80  
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe  
 85 90 95  
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu  
 100 105 110  
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly  
 115 120 125  
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro  
 130 135 140  
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile  
 145 150 155 160  
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val  
 165 170 175  
 Lys

## (2) INFORMATION FOR SEQ ID NO:5227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala  
1 5 10 15  
Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln  
20 25 30  
His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro  
35 40 45  
Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly  
50 55 60  
Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu  
65 70 75 80  
Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu  
85 90 95  
Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met  
100 105 110  
Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp  
115 120 125  
Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln  
130 135 140  
Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys  
145 150 155 160  
Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe  
165 170 175  
Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe  
180 185 190  
Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr  
195 200 205  
Cys

(2) INFORMATION FOR SEQ ID NO:5228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg  
 1 5 10 15  
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys  
 20 25 30  
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp  
 35 40 45  
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val  
 50 55 60  
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly  
 65 70 75 80  
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys  
 85 90 95  
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln  
 100 105 110  
 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala  
 115 120 125  
 25 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His  
 130 135 140  
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys  
 145 150 155 160  
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys  
 165 170 175  
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu  
 180 185 190  
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu  
 195 200 205  
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp  
 210 215 220  
 45 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu  
 225 230 235 240  
 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu  
 245 250 255

## (2) INFORMATION FOR SEQ ID NO:5229:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 246 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10

Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys  
 1 5 10 15

Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr  
 20 25 30

15

Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp  
 35 40 45

Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn  
 50 55 60

20

Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp  
 65 70 75 80

Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser  
 85 90 95

25

Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly  
 100 105 110

Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val  
 115 120 125

30

Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala  
 130 135 140

Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg  
 145 150 155 160

35

Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln  
 165 170 175

Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile  
 180 185 190

40

Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly  
 195 200 205

45

Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr  
 210 215 220

Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly  
 225 230 235 240

50

Leu Gly Ala Trp Gly Phe  
 245

55

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys Glu Pro His Lys Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser  
 1 5 10 15  
 Ala Ile Val Ala Thr Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala  
 20 25 30  
 Ile Thr His Glu Ser Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe  
 35 40 45  
 Asp Arg Ser His Gly Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp  
 50 55 60  
 Gly Ala Phe Ser Asp Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp  
 65 70 75 80  
 Val Lys Ala Ile Asp Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys  
 85 90 95  
 Ser Ser Lys Ile Phe Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu  
 100 105 110  
 Ser Glu Gln Ala Ala Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val  
 115 120 125  
 Val Phe Ile Ser Asp His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile  
 130 135 140  
 Asp Ser Ser Glu Ala Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp  
 145 150 155 160  
 Met Ser Lys Gly Met Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln  
 165 170 175  
 Gly Val Lys Ser Ser Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe  
 180 185 190  
 Arg Tyr Asn Ala Leu Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser  
 195 200 205  
 Lys Glu Ser Phe Gly Ile Thr Glu Gly Val Lys Ser Val Ser Met His  
 210 215 220  
 Ala Gly Ser Thr Leu Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile  
 225 230 235 240  
 Val Tyr Thr Pro Glu Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala  
 245 250 255



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Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr  
260 265 270

5 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp  
275 280 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn  
290 295 300

10 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly  
305 310 315 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly  
325 330 335

15 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu  
340 345 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro  
355 360 365

20 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe  
370 375 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn  
385 390 395 400

25 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe  
405 410 415

30 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile  
420 425 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val  
435 440 445

35 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys  
450 455 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys  
465 470 475 480

40 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu  
485 490 495

Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr  
500 505 510

45 Leu Ile Thr Thr Asp Phe Lys  
515

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
30	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
40	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	
55																				

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Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe  
290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys  
305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr  
1 5 10 15

Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr  
20 25 30

Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala  
35 40 45

Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu  
50 55 60

Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys  
65 70 75 80

Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu  
85 90 95

Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser  
100 105 110

Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp  
115 120 125

Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala  
130 135 140

Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe  
145 150 155 160

Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr  
165 170 175

His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe  
180 185 190

Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg  
195 200 205

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Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile  
 210 215 220  
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr  
 225 230 235 240  
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly  
 245 250 255  
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His  
 260 265 270  
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met  
 275 280 285  
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met  
 290 295 300  
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val  
 305 310 315 320  
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr  
 325 330 335  
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys  
 340 345 350  
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro  
 355 360 365  
 30 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His  
 370 375 380  
 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu  
 385 390 395 400  
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly  
 405 410 415  
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg  
 420 425 430  
 40 Lys

(2) INFORMATION FOR SEQ ID NO:5233:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

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Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val  
 1 5 10 15  
 Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly  
 5 20 25 30  
 Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys  
 35 40 45  
 Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile  
 10 50 55 60  
 Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu  
 65 70 75 80  
 Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu  
 15 85 90 95  
 Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr  
 100 105 110  
 Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys  
 115 120 125  
 Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile  
 130 135 140  
 Asp Ile Asn Val Lys Thr Lys  
 145 150

(2) INFORMATION FOR SEQ ID NO:5234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe  
 1 5 10 15  
 Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His  
 20 25 30  
 Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His  
 35 40 45  
 Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala  
 50 55 60  
 Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln  
 55 65 70 75 80

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Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn Val Gln Asn Glu Ala  
 85 90 95  
 5 Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser His Ser Thr Glu Ser  
 100 105 110  
 Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln His Glu Glu Glu Tyr  
 115 120 125  
 10 Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser His Pro Glu Pro Ile  
 130 135 140  
 Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn Ala Glu Asn Asn Thr  
 145 150 155 160  
 15 Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala Glu Gln Ser Gln Gln  
 165 170 175  
 Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln Ser Glu Thr Ser Lys  
 180 185 190  
 20 Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp Gln Asp Glu Pro Lys  
 195 200 205  
 25 Glu His His Asn Gly Lys Lys Ala Ala Ala Ile Gly Ala Gly Thr Ala  
 210 215 220  
 Gly Val Ala Gly Ala Ala Gly Ala Met Ala Ala Ser Lys Ala Lys Lys  
 225 230 235 240  
 30 His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser Gly Lys Ala Asn Asn  
 245 250 255  
 Ser Thr Glu Asp Lys Ala Ser Gln Asp Lys Ser Lys Asp His His Asn  
 260 265 270  
 35 Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr Ala Gly Leu Ala Gly  
 275 280 285  
 Gly Ala Ala Ser Lys Ser Ala Ser Ala Ala Ser Lys Pro His Ala Ser  
 290 295 300  
 40 Asn Asn Ala Ser Gln Asn His Asp Glu His Asp Asn His Asp Arg Asp  
 305 310 315 320  
 Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val Leu Leu Pro Leu Ile  
 325 330 335  
 45 Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile Phe Gly Gly Met Ala  
 340 345 350  
 Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn Lys Ile Ala Asn Thr  
 355 360 365  
 50 Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys Asp Thr Ser Lys Asp  
 370 375 380  
 55 Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser Asp Lys Ser Lys Glu  
 385 390 395 400

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Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn  
405 410 415

Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln  
420 425 430

Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln  
435 440 445

Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln  
450 455 460

Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala  
465 470 475 480

Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile  
485 490 495

Pro

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn  
1 5 10 15

Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr  
20 25 30

Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser  
35 40 45

Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile  
50 55 60

Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp  
65 70 75 80

Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn  
85 90 95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala  
100 105 110

Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe  
115 120 125

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Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe Phe Ser  
130 135 140

5 Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala Glu Val  
145 150 155 160

Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr  
165 170 175

10 Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser Pro Val  
180 185 190

Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly Thr Gln  
195 200 205

15 Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu Glu Thr  
210 215 220

Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr Asn Asp  
225 230 235 240

20 Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr Asn Asp  
245 250 255

Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Thr Ser Asn  
260 265 270

25 Gln Asn Ile Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln Ala Thr  
275 280 285

30 Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn Ala Asp  
290 295 300

Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly Asn Thr  
305 310 315 320

35 Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn Gln Gln  
325 330 335

Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn Pro Ala  
340 345 350

40 Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile Asp Phe  
355 360 365

Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Phe Tyr His Tyr Ala Ser  
370 375 380

45 Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro Ile Ile  
385 390 395 400

Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr  
405 410 415

50 Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp Ser Asp  
420 425 430

55 Lys Asp Tyr Ala Tyr Ile Arg Phe Pro Val Ser Asn Gly Thr Arg Glu  
435 440 445



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	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490						495	
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
		530					535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570						575	
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
		610					615					620					
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
		625				630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
				645						650					655		
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660				665						670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680					685				
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
45		690				695						700					
	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
		705				710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
			740					745						750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
			755					760					765				

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Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met  
770 775 780

5 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys  
785 790 795 800

Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys  
805 810 815

10 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys  
820 825 830

Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys  
835 840 845

15 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser  
850 855 860

Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg  
865 870 875 880

20 Asn Asn Xaa Gln Ala Asn  
885

(2) INFORMATION FOR SEQ ID NO:5236:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 236 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
30 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile  
1 5 10 15

40 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser  
20 25 30

Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys  
35 40 45

45 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val  
50 55 60

50 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn  
65 70 75 80

Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys  
85 90 95

55 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys  
100 105 110

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Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu  
115 120 125

Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys  
130 135 140

Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr  
145 150 155 160

Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly  
165 170 175

Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser  
180 185 190

Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly  
195 200 205

Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro  
210 215 220

Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys  
225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr  
1 5 10 15

Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr  
20 25 30

Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val  
35 40 45

Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly  
50 55 60

Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr  
65 70 75 80

Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala  
85 90 95

Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr  
100 105 110

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Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr  
 115 120 125  
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser  
 130 135 140  
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln  
 145 150 155 160  
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu  
 165 170 175  
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln  
 180 185 190  
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val  
 195 200 205  
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu  
 210 215 220  
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val  
 225 230 235 240  
 25 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile  
 245 250 255  
 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile  
 260 265 270  
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr  
 275 280 285  
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu  
 290 295 300  
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser  
 305 310 315 320  
 40 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu  
 325 330 335  
 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly  
 340 345 350  
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys  
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val  
 1 5 10 15  
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala  
 20 25 30  
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser  
 35 40 45  
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn  
 50 55 60  
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys  
 65 70 75 80  
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile  
 85 90 95  
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr  
 100 105 110  
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr  
 115 120 125  
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn  
 130 135 140  
 Val Asp Thr Lys Lys Gln  
 145 150  
 30

## (2) INFORMATION FOR SEQ ID NO:5239:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp  
 1 5 10 15  
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly  
 20 25 30  
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile  
 35 40 45  
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly  
 50 55 60

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Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met  
65 70 75 80

Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu  
5 85 90 95

Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr  
100 105 110

Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser  
10 115 120 125

Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys  
130 135 140

Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu  
15 145 150 155 160

Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser  
165 170 175

Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val  
20 180 185 190

Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile  
25 195 200 205

Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr  
210 215 220

Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu  
30 225 230 235

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 133 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val  
1 5 10 15

Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser  
50 20 25 30

Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys  
35 40 45

Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val  
55 50 55 60

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Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu  
65 70 75 80  
Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys  
85 90 95  
Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe  
100 105 110  
Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu  
115 120 125  
Phe Asp Val Lys Ala  
130

(2) INFORMATION FOR SEQ ID NO:5241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 508 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val  
1 5 10 15  
Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly  
20 25 30  
Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro  
35 40 45  
Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp  
50 55 60  
Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser  
65 70 75 80  
Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp  
85 90 95  
Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn  
100 105 110  
Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala  
115 120 125  
Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly  
130 135 140  
Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu  
145 150 155 160

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Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Phe Pro Met Leu  
165 170 175

5 Leu Ala Ala Trp Lys Ile Ala Pro Ala Ile Ala Ala Gly Asn Thr Ile  
180 185 190

Val Ile Gln Pro Ser Ser Ser Thr Pro Leu Ser Leu Leu Glu Val Ala  
195 200 205

10 Lys Ile Phe Gln Glu Val Leu Pro Lys Gly Val Val Asn Ile Leu Thr  
210 215 220

Gly Lys Gly Ser Glu Ser Gly Asn Ala Ile Phe Asn His Asp Gly Val  
225 230 235 240

15 Asp Lys Leu Ser Phe Thr Gly Ser Thr Asp Val Gly Tyr Gln Val Ala  
245 250 255

Glu Ala Ala Ala Lys His Leu Val Pro Ala Thr Leu Glu Leu Gly Gly  
260 265 270

20 Lys Ser Ala Asn Ile Ile Leu Asp Asp Ala Asn Leu Asp Leu Ala Val  
275 280 285

Glu Gly Ile Gln Leu Gly Ile Leu Phe Asn Gln Gly Glu Val Cys Ser  
290 295 300

25 Ala Gly Ser Arg Leu Leu Val His Glu Lys Ile Tyr Asp Gln Leu Val  
305 310 315 320

30 Pro Arg Leu Gln Glu Ala Phe Ser Asn Ile Lys Val Gly Asn Pro Gln  
325 330 335

Asp Glu Ala Thr Gln Met Gly Ser Gln Thr Gly Lys Asp Gln Leu Asp  
340 345 350

35 Lys Ile Gln Ser Tyr Ile Asp Ala Ala Lys Glu Ser Asp Ala Gln Ile  
355 360 365

Leu Ala Gly Gly His Arg Leu Thr Glu Asn Gly Leu Asp Lys Gly Phe  
370 375 380

40 Phe Phe Glu Pro Thr Leu Ile Ala Val Pro Asp Asn His His Lys Leu  
385 390 395 400

Ala Gln Glu Glu Ile Phe Gly Pro Val Leu Thr Val Ile Lys Val Lys  
405 410 415

45 Asp Asp Gln Glu Ala Ile Asp Ile Ala Asn Asp Ser Glu Tyr Gly Leu  
420 425 430

Ala Gly Gly Val Phe Ser Gln Asn Ile Thr Arg Ala Leu Asn Ile Ala  
435 440 445

50 Lys Ala Val Arg Thr Gly Arg Ile Trp Ile Asn Thr Tyr Asn Gln Val  
450 455 460

55 Pro Glu Gly Ala Pro Phe Gly Gly Tyr Lys Lys Ser Gly Ile Gly Arg  
465 470 475 480



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Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile  
485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr  
500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
1 5 10 15  
Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
20 25 30  
Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
35 40 45  
Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
50 55 60  
Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
65 70 75 80  
Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
85 90 95  
Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
100 105 110  
Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
115 120 125  
Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
130 135 140  
Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
145 150 155 160  
Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
165 170 175  
Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
180 185 190  
Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
195 200 205

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Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val  
210 215 220

5 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly  
225 230 235 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn  
245 250 255

10 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val  
260 265 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys  
275 280 285

15 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr  
290 295 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp  
305 310 315 320

20 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly  
325 330 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu  
340 345 350

25 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr  
355 360 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly  
370 375 380

30 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro  
385 390 395 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn  
405 410 415

35 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu  
420 425 430

40 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr  
435 440 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr  
450 455 460

45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly  
465 470 475 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp  
485 490 495

50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr  
500 505 510

Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser  
515 520 525

55

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:5243:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 274 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln  
 1 5 10 15  
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln  
 20 25 30  
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly  
 25 35 40 45  
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp  
 50 55 60  
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe  
 30 65 70 75 80  
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln  
 85 90 95  
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala  
 35 100 105 110  
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr  
 115 120 125  
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser  
 40 130 135 140  
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala  
 145 150 155 160  
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val  
 45 165 170 175  
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser  
 180 185 190  
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr  
 195 200 205  
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu  
 55 210 215 220

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His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val  
225 230 235 240  
Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro  
245 250 255  
Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn  
260 265 270  
Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val  
1 5 10 15  
Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile  
20 25 30  
Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly  
35 40 45  
Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr  
50 55 60  
Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe  
65 70 75 80  
Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys  
85 90 95  
Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys  
100 105 110  
Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val  
115 120 125  
Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr  
130 135 140  
Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr  
145 150 155 160  
Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu  
165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu  
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser  
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr  
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser  
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr  
245 250 255

15 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile  
260 265 270

Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn  
275 280 285

20 Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly  
290 295 300

Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser  
305 310 315 320

25 Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys  
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala  
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln  
355 360 365

35 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp  
370 375 380

Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp  
385 390 395 400

40 Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp  
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr  
420 425 430

## (2) INFORMATION FOR SEQ ID NO:5245:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 469 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe	100	105	110	
	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
25	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
30	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
35	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
45	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
50	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

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Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr  
305 310 315 320

5 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp  
325 330 335

Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr  
340 345 350

10 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val  
355 360 365

Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu  
370 375 380

15 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr  
385 390 395 400

Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser  
405 410 415

20 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn  
420 425 430

25 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln  
435 440 445

Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe  
450 455 460

30 Gly Gly Asp Ile Ile  
465

(2) INFORMATION FOR SEQ ID NO:5246:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 414 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala  
1 5 10 15

Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala  
20 25 30

Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu  
35 40 45

55 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu  
50 55 60

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Asn Ile Tyr Arg Arg Leu Thr Asp Ser Glu Glu Gln Leu Lys Gly Glu  
 65 70 75 80  
 5 Asn Leu Ile Ile Ser Ala Thr Thr Glu Val Phe Lys Pro Ile Met Ser  
 85 90 95  
 Ser Thr Leu Val Thr Ile Ile Val Phe Leu Pro Leu Val Phe Val Ser  
 100 105 110  
 10 Gly Ser Val Gly Glu Met Phe Arg Pro Phe Ala Leu Ala Ile Ala Phe  
 115 120 125  
 Ser Leu Leu Ala Ser Leu Leu Val Ser Ile Thr Leu Val Pro Ala Leu  
 130 135 140  
 15 Ala Ala Thr Leu Phe Lys Lys Gly Val Lys Arg Arg Asn Lys Gln His  
 145 150 155 160  
 Gln Glu Gly Leu Gly Val Val Ser Thr Thr Tyr Lys Lys Val Leu His  
 165 170 175  
 20 Trp Ser Leu Asn His Lys Trp Ile Val Ile Ile Leu Ser Thr Leu Ile  
 180 185 190  
 Leu Val Ala Thr Ile Val Phe Gly Gly Pro Arg Leu Gly Thr Ser Phe  
 195 200 205  
 25 Ile Ser Ala Gly Asp Asp Lys Phe Leu Ala Ile Thr Tyr Thr Pro Lys  
 210 215 220  
 30 Pro Gly Glu Thr Glu Gln Ala Val Leu Asn His Ala Lys Asp Val Glu  
 225 230 235 240  
 Lys Tyr Leu Lys Gln Lys Lys His Val Lys Thr Ile Gln Tyr Ser Val  
 245 250 255  
 35 Gly Gly Ser Ser Pro Val Asp Pro Thr Gly Ser Thr Asn Ser Met Ala  
 260 265 270  
 Ile Met Val Glu Tyr Asp Asn Asp Thr Pro Asn Phe Asp Val Glu Ala  
 275 280 285  
 40 Asp Lys Val Ile Lys His Ala Asp Gly Phe Lys His Pro Gly Glu Trp  
 290 295 300  
 Lys Asn Gln Asp Leu Gly Thr Gly Ala Gly Asn Lys Ser Val Glu Val  
 305 310 315 320  
 45 Thr Val Lys Gly Pro Ser Met Asp Ala Ile Lys Ser Thr Val Lys Asp  
 325 330 335  
 50 Ile Glu Gln Lys Met Lys Gln Val Lys Gly Leu Ala Asn Val Lys Ser  
 340 345 350  
 Asp Leu Ser Gln Thr Tyr Asp Gln Tyr Glu Ile Lys Val Asp Gln Asn  
 355 360 365  
 55 Lys Ala Ala Glu Asn Gly Ile Ser Ala Ser Gln Leu Ala Met His Leu  
 370 375 380



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Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly  
385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala  
405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu  
1 5 10 15  
Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu  
20 25 30  
Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile  
35 40 45  
Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp  
50 55 60  
Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val  
65 70 75 80  
Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys  
85 90 95  
His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile  
100 105 110  
Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro  
115 120 125  
Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro  
130 135 140  
Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu  
145 150 155 160  
Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe  
165 170 175  
Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn  
180 185 190  
Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu  
195 200 205

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Lys Leu Phe Asn Arg Thr Glu Gln Thr Glu Lys His Ile Tyr Asp Asp  
 210 215 220  
 5 Ser Thr Gln Phe Arg Thr Leu Thr Met Arg Ile Leu Arg Ser Ala Phe  
 225 230 235 240  
 Leu Ser Gly Leu Met Leu Glu Phe Ile Ser Met Leu Gly Ile Gly Leu  
 245 250 255  
 10 Val Ala Leu Glu Ala Thr Leu Ser Leu Val Val Phe His Asn Ile Asp  
 260 265 270  
 Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn  
 275 280 285  
 15 Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr Gly Lys Gln Ser Glu  
 290 295 300  
 Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn  
 305 310 315 320  
 20 Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln  
 325 330 335  
 Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu  
 340 345 350  
 25 Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val  
 355 360 365  
 Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly  
 370 375 380  
 30 Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu  
 385 390 395 400  
 35 Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile  
 405 410 415  
 Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu  
 420 425 430  
 40 Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr  
 435 440 445  
 Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly  
 450 455 460  
 45 Gly Gln Met Arg Arg Ile Glu Leu Cys Arg Leu Leu Val Met Lys Pro  
 465 470 475 480  
 Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr  
 485 490 495  
 50 Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr  
 500 505 510  
 55 Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg  
 515 520 525

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Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile  
530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu  
545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe  
1 5 10 15  
Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu  
20 25 30  
Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met  
35 40 45  
Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr  
50 55 60  
Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr  
65 70 75 80  
Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp  
85 90 95  
Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val  
100 105 110  
Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala  
115 120 125  
Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val  
130 135 140  
Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile  
145 150 155 160  
Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu  
165 170 175  
Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr  
180 185 190  
Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp  
195 200 205

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Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe  
 210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val  
 225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly  
 245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu  
 260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala  
 275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr  
 290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn  
 305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr  
 325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn  
 340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg  
 355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn  
 370 375 380

Gln Ile Asn Gln Ile Met Gln Tyr Lys  
 385 390

(2) INFORMATION FOR SEQ ID NO:5249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 936 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu  
 1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val  
 20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala  
 35 40 45

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	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	Ser	Ala	Ser	Asn	Glu	Ser	Lys	
	50						55					60					
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr	
	65					70				75					80		
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr	
					85					90					95		
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser	
				100				105						110			
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr	
				115				120						125			
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn	
				130				135					140				
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser	
	145					150					155					160	
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr	
					165					170					175		
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr	
25				180					185					190			
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys	
				195				200					205				
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala	
		210					215					220					
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp	
	225					230					235					240	
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr	
					245					250					255		
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe	
				260					265					270			
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val	
				275				280					285				
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro	
		290					295					300					
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser	
		305				310					315				320		
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp	
50					325					330					335		
	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn	
				340					345					350			
55	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr	
				355				360					365				

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Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe  
370 375 380

5 Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn  
385 390 395 400

Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val  
405 410 415

10 Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn  
420 425 430

Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp  
435 440 445

15 Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe  
450 455 460

Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln  
465 470 475 480

20 Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr  
485 490 495

Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu  
500 505 510

25 Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg  
515 520 525

Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser  
530 535 540

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro  
545 550 555 560

35 Gly Glu Ile Glu Pro Ile Pro Glu Asp Ser Asp Ser Asp Pro Gly Ser  
565 570 575

Asp Ser Gly Ser Asp Ser Asn Ser Asp Ser Gly Ser Asp Ser Gly Ser  
580 585 590

40 Asp Ser Thr Ser Asp Ser Gly Ser Asp Ser Ala Ser Asp Ser Asp Ser  
595 600 605

Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser  
610 615 620

45 Asp Ser Ala Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp Ser Asp Ser  
625 630 635 640

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
645 650 655

50 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
660 665 670

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
675 680 685

55

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	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	690	695	700
5	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	705	710	715
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	725	730	735
10	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	740	745	750
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	755	760	765
15	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Ser	770	775	780
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	785	790	795
20	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	805	810	815
25	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	820	825	830
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Gly	Ser	835	840	845
30	Asp	Ser	Asp	Ser	Ser	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asn	Ser	850	855	860
	Asp	Ser	Glu	Ser	Val	Ser	Asn	Asn	Asn	Val	Val	Pro	Pro	Asn	Ser	Pro	865	870	875
35	Lys	Asn	Gly	Thr	Asn	Ala	Ser	Asn	Lys	Asn	Glu	Ala	Lys	Asp	Ser	Lys	885	890	895
40	Glu	Pro	Leu	Pro	Asp	Thr	Gly	Ser	Glu	Asp	Glu	Ala	Asn	Thr	Ser	Leu	900	905	910
	Ile	Trp	Gly	Leu	Leu	Ala	Ser	Ile	Gly	Ser	Leu	Leu	Leu	Phe	Arg	Arg	915	920	925
45	Lys	Lys	Glu	Asn	Lys	Asp	Lys	Lys									930	935	

(2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys  
 65 70 75 80  
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr  
 85 90 95  
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn  
 100 105 110  
 Leu Lys His Lys Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys  
 115 120 125  
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys  
 130 135 140  
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala  
 145 150 155 160  
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln  
 165 170 175  
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys  
 180 185 190  
 Ile Leu

## (2) INFORMATION FOR SEQ ID NO:5251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55 Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp  
 1 5 10 15



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Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser  
 20 25 30  
 5 Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr  
 35 40 45  
 Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His  
 50 55 60  
 10 Leu Phe Gly Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys  
 65 70 75 80  
 Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp  
 85 90 95  
 15 Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu  
 100 105 110  
 Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile  
 115 120 125  
 20 Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala  
 130 135 140  
 25 Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu  
 145 150 155 160  
 Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys  
 165 170 175  
 30 His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly  
 180 185 190  
 Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser  
 195 200 205  
 35 Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu  
 210 215 220  
 Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp  
 225 230 235 240  
 40 Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile  
 245 250 255  
 Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn  
 260 265 270  
 45 Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His  
 275 280 285  
 50 Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly  
 290 295 300  
 Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu  
 305 310 315 320  
 55 Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile  
 325 330 335

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His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys  
340 345 350

Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe  
355 360 365

Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile  
370 375 380

Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His  
385 390 395 400

Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His  
405 410 415

Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val  
420 425 430

Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro  
435 440 445

Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro  
450 455 460

Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala  
465 470 475 480

Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val  
485 490 495

Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro  
500 505 510

Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly  
515 520 525

Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile  
530 535 540

Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala  
545 550 555

(2) INFORMATION FOR SEQ ID NO:5252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 251 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu  
1 5 10 15

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Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val  
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn  
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp  
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu  
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro  
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile  
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys  
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr  
130 135 140

25 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu  
145 150 155 160

Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg  
165 170 175

30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys  
180 185 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln  
195 200 205

35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys  
210 215 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser  
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala  
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

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1 Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 10 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu  
 15 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser  
 20 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp  
 25 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser  
 30 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys  
 35 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys  
 40 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser  
 45 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln  
 50 Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1027 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

1 Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 10 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu  
 15 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn  
 20

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Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu  
 65 70 75 80  
 5 Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala  
 85 90 95  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln  
 100 105 110  
 10 Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys  
 115 120 125  
 Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn  
 130 135 140  
 15 Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln  
 145 150 155 160  
 Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala  
 165 170 175  
 20 Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala  
 180 185 190  
 Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser  
 195 200 205  
 25 Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn  
 210 215 220  
 Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu  
 225 230 235 240  
 Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu  
 245 250 255  
 35 Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro  
 260 265 270  
 Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu  
 275 280 285  
 40 Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val  
 290 295 300  
 Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr  
 305 310 315 320  
 45 Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu  
 325 330 335  
 Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn  
 340 345 350  
 50 Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn  
 355 360 365  
 55 Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr  
 370 375 380

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Thr Ser Val Thr Val Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn  
385 390 395 400

5 Gly Asn Gln Pro Lys Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu  
405 410 415

Asp Ile Ala Lys Ser Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe  
420 425 430

10 Lys Glu Val Thr Ser Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn  
435 440 445

Gly Ser Tyr Ser Leu Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val  
450 455 460

15 His Tyr Asp Gly Glu Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg  
465 470 475 480

Thr Gln Met Val Gly His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp  
485 490 495

20 Arg Gly Tyr Thr Leu Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn  
500 505 510

Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys  
515 520 525

25 Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr  
530 535 540

Asp Lys Asn Leu Val Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr  
545 550 555 560

30 Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Gly Tyr Val  
565 570 575

35 Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp  
580 585 590

Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly  
595 600 605

40 Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser  
610 615 620

Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu  
625 630 635 640

45 Asp Thr Asn Pro Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val  
645 650 655

Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser  
660 665 670

50 Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn  
675 680 685

55 Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln Ala Gln  
690 695 700

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	Gly	Pro	Val	Glu	Glu	Ile	Thr	Lys	Asn	Asn	His	His	Ile	Ser	His	Ser	705		710		715		720
5	Gly	Leu	Gly	Thr	Glu	Asn	Gly	His	Gly	Asn	Tyr	Asp	Val	Ile	Glu	Glu		725		730		735	
	Ile	Glu	Glu	Asn	Ser	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu		740		745		750	
10	Gly	Gly	Gln	Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu		755		760		765	
	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe		770		775		780	
15	Asp	Ser	Val	Pro	Gln	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe		785		790		795	
	Glu	Glu	Asp	Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn		805		810		815	
20	Ile	Ile	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn		820		825		830	
	Lys	His	Thr	Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser		835		840		845	
25	Tyr	Gln	Phe	Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu		850		855		860	
	Pro	Lys	Val	Ser	Gly	Gln	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp		865		870		875	
30	Thr	Thr	Pro	Pro	Ile	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro		885		890		895	
	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu		900		905		910	
35	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu		915		920		925	
40	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro		930		935		940	
	Val	Pro	Pro	Ala	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu		945		950		955	
45	Gln	Gly	Lys	Val	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys		965		970		975	
	Ala	Val	Ala	Pro	Thr	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu	Leu	Pro		980		985		990	
50	Glu	Thr	Gly	Gly	Glu	Glu	Ser	Thr	Asn	Lys	Gly	Met	Leu	Phe	Gly	Gly		995		1000		1005	
	Leu	Phe	Ser	Ile	Leu	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys	Lys	Asn		1010		1015		1020	
55																							

His Lys Ala  
1025

(2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys  
1 5 10 15  
Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu  
20 25 30  
Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys  
35 40 45  
Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp  
50 55 60  
Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu  
65 70 75 80  
Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val  
85 90 95  
Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys  
100 105 110  
Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys  
115 120 125  
Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys  
130 135 140  
Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg  
145 150 155

Claims

1. Computer readable medium having recorded thereon a nucleotide sequence of the *Staphylococcus aureus* genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

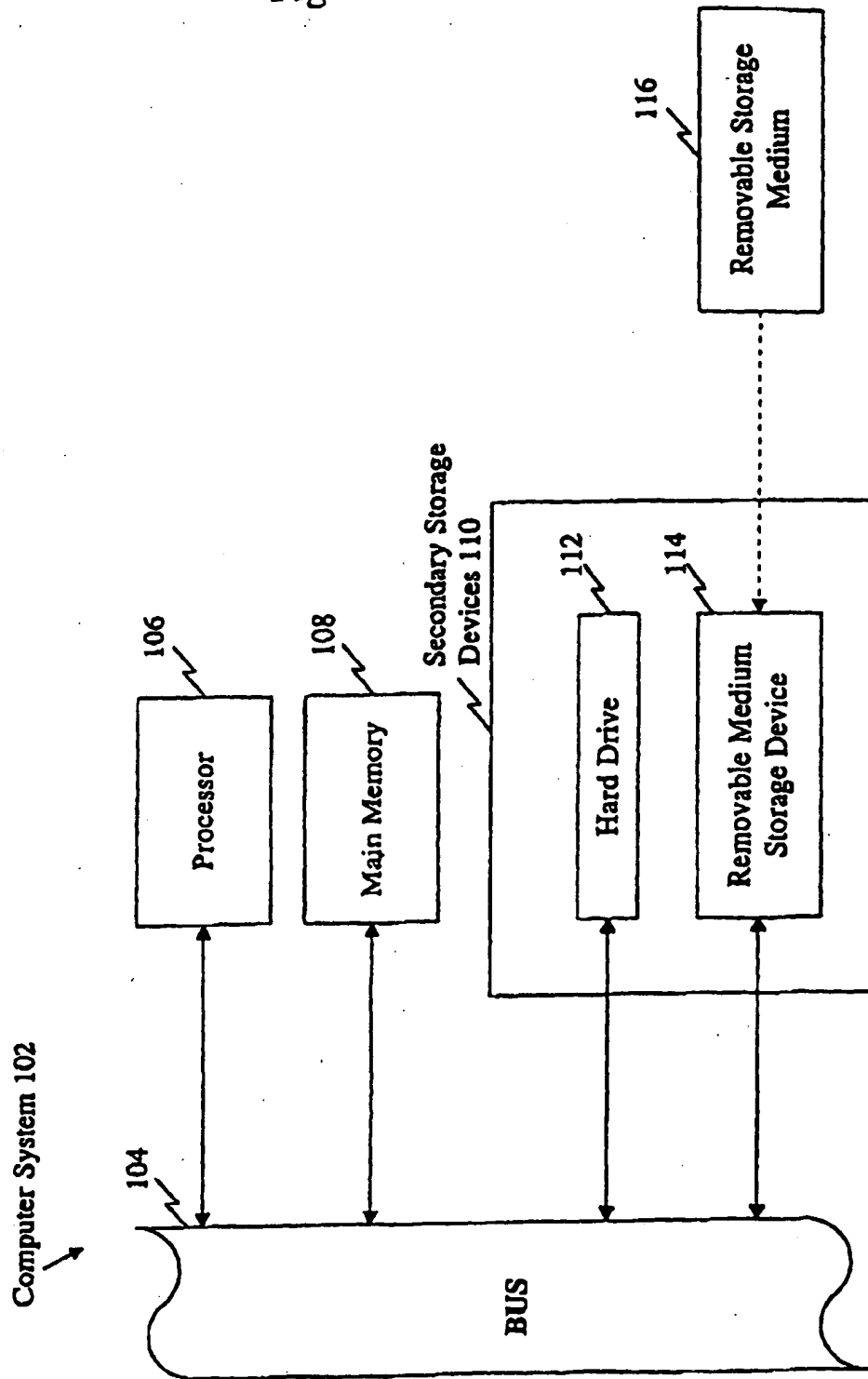


3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 5 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
  - 10 (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;
  - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
  - 15 (c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 20 7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
- 25 8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
- 30 9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
11. A vector comprising a fragment of claim 8.
- 35 12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 40 13. A vector comprising a fragment of claim 12.
- 45 14. A organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
- 50 15. A method for producing a polypeptide in a host cell comprising the steps of:
  - 55 (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
  - (b) isolating said protein.
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
  - (b) identifying members of said library which contain sequences that hybridize to said target sequence;
  - (c) isolating the nucleic acid molecules from said members identified in step (b).
19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) isolating mRNA, DNA, or cDNA produced from an organism;
  - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
  - (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8.
21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
  - (a) an isolated polypeptide antigen of claim 24, and
  - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1



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